

Copyright (c) 1993 - 2006 Biocceleration Ltd.	Gencore version 5.1.8	25	106	100.0	498	7	AAE38507	Human ang	
			26	106	100.0	498	7	AAE38501	Human ang
			27	106	100.0	498	7	AAE38499	Mouse ang
			28	106	100.0	498	7	AAE38486	Human ang
			29	106	100.0	498	7	AAE38497	Mouse ang
			30	106	100.0	498	7	ADD6265	Human ang
			31	106	100.0	498	7	ADF7296	Human ang
			32	106	100.0	498	7	ADQ19778	Human sof
			33	106	100.0	498	8	ADR87338	Amino aci
			34	106	100.0	498	8	ADS13782	Mouse ang
			35	106	100.0	498	8	ADS13781	Human ang
			36	106	100.0	498	9	ADZ80187	Human TIE
			37	106	100.0	498	9	AEA81247	Human ang
			38	106	100.0	498	9	AEB87159	Human Ang
			39	96	90.6	495	3	AYY78807	Angiopoie
			40	96	90.6	495	3	AYY78804	Angiopoie
			41	96	90.6	495	3	AAB28393	Human ang
			42	96	90.6	495	5	AAU77945	Amino aci
			43	96	90.6	498	7	AAE38493	BIG angio
			44	96	90.6	498	7	ADS13806	Ang-1 Lin
			45	89.5	84.4	89.5	7	AAE38508	Human ang
Run on:	May 11, 2006, 11:29:52 ; Search time 184 Seconds								
	(without alignments)								
	47.759 Million cell updates/sec								
Title:	US-10-789-2222-1								
Perfect score:	106								
Sequence:	1 LCTKGVLLKGKREBEKPF 20								
Scoring table:	BLOSUM62								
Scoring table:	Gapext 10.0 , Gapext 0.5								
searched:	2443133 seqs, 439378781 residues								
	total number of hits satisfying chosen parameters:								
	2443163								

related to lack of blood vessels such as ischaemia in hearts and limbs; to reduce stroke, heart attack, blood vessel blockage, haemorrhage, atherosclerosis risk by maintaining the health and integrity of blood vessels; to assist the recovery of the patients who had stroke and the angioplasty procedure by promoting the growth/survival of endothelial cells and establish endothelial monolayer and inhibit excessive inflammation, haemorrhage, and proliferation of vascular smooth muscle; to treat patients with restenosis by inhibiting re-closure of blood vessel after inserting stents into blood vessels; to make stable and functional artificial blood vessels comprising using the composition above; of identifying compounds that modulates binding of Ang-1 to ECM; of treating an individual suspected of having cancer; of preventing diabetes and/or arthritis in an individual suspected of being at risk of developing diabetes or arthritis. The pharmaceutical composition is useful for treating diseases and disorders, e.g. cancer, coronary artery disease, vascular disease, ischaemia, restenosis, diabetes, stroke, angiogenesis, or arthritis. The present sequence represents an ECM-binding fragment of Ang-1 protein.

XX Sequence 20 AA;

Query Match 100.0%; Score 106; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.9e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGKGRREEKPF 20  
Db 1 LCTKEGVLLKGKGRREEKPF 20

RESULT 2  
ID ADS13769  
AC ADS13769 Standard; peptide; 20 AA.

XX ADS13769;

XX DT 02-DEC-2004 (first entry)

XX Human Ang-1 protein ECM-binding fragment.

KW Ang-1; extracellular matrix; ECM; angiopoietin; cytostatic; vasotropic; antidiabetic; antiarthritis; cerebroprotective; antiangiogenic; gene therapy; human.

XX Homo sapiens.

XX PN WO2004076650-A2.

XX PD 10-SEP-2004.

XX PF 27-FEB-2004; 2004WO-US006101.

XX PR 27-FEB-2003; 2003US-0450582P.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX PI Yu Q;

XX WPI; 2004-653413/63.

DR N-PDB; ADS13787.

XX DR WPI; 2004-653413/63.

New pharmaceutical composition comprises a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or ischaemia. The invention relates to a pharmaceutical composition comprising a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of angiopoietin (Ang-1) protein or a mutant Ang-1. Also provided are methods of treating an individual suspected of having coronary artery disease, vascular disease or a condition involving

CC ischaemia; of promoting angiogenesis, endothelial survival and maintaining vascular integrity in an individual; of treating an individual suspected of having a disease related to lack of blood vessels; to effectively promote angiogenesis in the patients with the diseases related to lack of blood vessels such as ischaemia in hearts and limbs; to reduce stroke, heart attack, blood vessel blockage, haemorrhage, atherosclerosis risk by maintaining the health and integrity of blood vessels; to assist the recovery of the patients who had stroke and the angioplasty procedure by promoting the growth/survival of endothelial cells and establish endothelial monolayer and inhibit excessive inflammation, haemorrhage, and proliferation of vascular smooth muscle; to treat patients with restenosis by inhibiting re-closure of blood vessels after inserting stents into blood vessels; to make stable and functional artificial blood vessels comprising using the composition above; of identifying compounds that modulates binding of Ang-1 to ECM; of treating an individual suspected of having cancer; of preventing diabetes and/or arthritis in an individual suspected of being at risk of developing diabetes or arthritis. The pharmaceutical composition is useful for treating diseases and disorders, e.g. cancer, coronary artery disease, vascular disease, ischaemia, restenosis, diabetes, stroke, angiogenesis, or arthritis. The present sequence represents an ECM-binding fragment of Ang-1 protein.

XX Sequence 20 AA;

Query Match 100.0%; Score 106; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.9e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LCTKEGVLLKGKGRREEKPF 20  
Db 1 LCTKEGVLLKGKGRREEKPF 20

RESULT 3

ADS13805

ID ADS13805 standard; peptide; 26 AA.

XX ADS13805;

XX DT 02-DEC-2004 (first entry)

XX DE 02-DEC-2004 (first entry)

XX DS Ang-1 linker peptide region.

XX Ang-1; extracellular matrix; ECM; angiopoietin; cytostatic; vasotropic; antidiabetic; antiarthritis; cerebroprotective; antiangiogenic; gene therapy. XX KW KW KW KW KW gene therapy.

XX OS Homo sapiens.

XX PN WO2004076650-A2.

XX PR 27-FEB-2003; 2003US-0450582P.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX PI Yu Q;

XX WPI; 2004-653413/63.

DR N-PDB; ADS13787.

XX DR WPI; 2004-653413/63.

New pharmaceutical composition comprises a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or ischaemia. The invention relates to a pharmaceutical composition comprising a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-

PS Example 1; Page 27; 114pp; English.

XX CC The invention relates to a pharmaceutical composition comprising a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-

binding fragment of angiopoietin (Ang)-1 protein or a mutant Ang-1. Also provided are methods of treating an individual suspected of having coronary artery disease, vascular disease or a condition involving ischaemia; of promoting angiogenesis, endothelial survival and maintaining vascular integrity in an individual; of treating an individual suspected of having a disease related to lack of blood vessels to effectively promote angiogenesis in the patients with the diseases related to lack of blood vessels such as ischaemia in hearts and limbs; to reduce stroke, heart attack, blood vessel blockage, haemorrhage, arteriosclerosis risk by maintaining the health and integrity of blood vessels; to assist the recovery of the patients who had stroke and the angioplasty procedure by promoting the growth/survival of endothelial cells and establish endothelial monolayer and inhibit excessive inflammation, haemorrhage, and proliferation of vascular smooth muscle; to treat patients with restenosis by inhibiting re-closure of blood vessel after inserting stents into blood vessels; to make stable and functional artificial blood vessels comprising using the composition above; of identifying compounds that modulates binding of Ang-1 to ECM; of treating an individual suspected of having cancer; of preventing diabetes and/or arthritis in an individual suspected of being at risk of developing diabetes or arthritis. The pharmaceutical composition is useful for treating diseases and disorders, e.g. cancer, coronary artery disease, vascular disease, ischaemia, restenosis, diabetes, stroke, angiogenesis, or arthritis. The present sequence represents a linker peptide region of Ang-1 protein.

Sequence 26 AA;

Query Match 100.0%; Score 106; DB 8; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 LCTREGVLLKGGRBEEKPP 26

Query Match 100.0%; Score 106; DB 8; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 LCTREGVLLKGGRBEEKPP 26

Query Match 100.0%; Score 106; DB 8; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 LCTREGVLLKGGRBEEKPP 26

Query Match 100.0%; Score 106; DB 8; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 LCTREGVLLKGGRBEEKPP 26

Query Match 100.0%; Score 106; DB 8; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 LCTREGVLLKGGRBEEKPP 26

Query Match 100.0%; Score 106; DB 8; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 LCTREGVLLKGGRBEEKPP 26

Query Match 100.0%; Score 106; DB 8; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 LCTREGVLLKGGRBEEKPP 26

Query Match 100.0%; Score 106; DB 8; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 LCTREGVLLKGGRBEEKPP 26

Query Match 100.0%; Score 106; DB 8; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 LCTREGVLLKGGRBEEKPP 26

Query Match 100.0%; Score 106; DB 8; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 LCTREGVLLKGGRBEEKPP 26

Query Match 100.0%; Score 106; DB 8; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 LCTREGVLLKGGRBEEKPP 26

binding fragment of angiopoietin (Ang)-1 protein or a mutant Ang-1. Also provided are methods of treating an individual suspected of having coronary artery disease, vascular disease or a condition involving ischaemia; of promoting angiogenesis, endothelial survival and maintaining vascular integrity in an individual; of treating an individual suspected of having a disease related to lack of blood vessels to effectively promote angiogenesis in the patients with the diseases related to lack of blood vessels such as ischaemia in hearts and limbs; to reduce stroke, heart attack, blood vessel blockage, haemorrhage, arteriosclerosis risk by maintaining the health and integrity of blood vessels; to assist the recovery of the patients who had stroke and the angioplasty procedure by promoting the growth/survival of endothelial cells and establish endothelial monolayer and inhibit excessive inflammation, haemorrhage, and proliferation of vascular smooth muscle; to treat patients with restenosis by inhibiting re-closure of blood functional artificial blood vessels comprising using the composition above; of identifying compounds that modulates binding of Ang-1 to ECM; of treating an individual suspected of having cancer; of preventing diabetes and/or arthritis in an individual suspected of being at risk of developing diabetes or arthritis. The pharmaceutical composition is useful for treating diseases and disorders, e.g. cancer, coronary artery disease, vascular disease, ischaemia, restenosis, diabetes, stroke, angiogenesis, or arthritis. The present sequence represents a linker peptide region of Ang-1 protein.

Sequence 235 AA;

Query Match 100.0%; Score 106; DB 6; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1.2e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTREGVLLKGGRBEEKPP 20

Db 215 LCTREGVLLKGGRBEEKPP 234

RESULT 5

AD123636 standard; protein; 261 AA.

ID AD123636

XX AD123636;

AC DT 22-APR-2004 (first entry)

XX DE Human Ang-1 fibrinogen-like domain/Preprotrypsin signal.

XX KW Human; Ang-1; fibrinogen-like domain; Preprotrypsin signal;

KW angiopoietin; coiled-coil domain; cell growth; proliferation;

KW matrix protein; transcription factor; growth factor; secretory protein;

KW cartilage matrix protein; CMP; cartilage oligomeric matrix protein; COMP;

KW Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell;

KW endothelial precursor cell.

XX OS Homo sapiens.

OS Synthetic.

XX PN US2003220476-A1.

XX PD 27-NOV-2003.

XX PP 18-OCT-2002; 2002US-00273180.

XX PR 21-MAY-2002; 2002US-0382541P.

XX PA (KOHG/) KOH G Y.

XX PI Koh GY;

XX DR WPI: 2004-010889/01.

XX DR N-PSDB; AD123635.

PT New coiled coil chimeric molecule comprising a coiled-coil domain linked

PT to either a receptor binding domain of ligand or ligand binding domain of

PT a receptor, useful for inhibiting or promoting differential function.

XX Disclosure; SEQ ID NO 2; 38pp; English.

CC The invention relates to a coiled coil chimeric molecule comprising a

CC coiled-coil domain linked to either a receptor binding domain of a ligand

CC or ligand binding domain of a receptor, which forms a biologically active

CC multimer, and where the chimaeric molecule in its non-multimeric form is

CC not biologically active. Also included are an isolated nucleic acid

CC encoding the coiled coil chimaeric molecule, an expression vector

CC

CC

CC

CC

CC

CC

CC

CC

CC

comprising the nucleic acid, a host cell comprising the vector, a soluble biologically active multimer comprising the coiled coil chimeric molecule, promoting cell growth or proliferation, decreasing or inhibiting ligand activity or cell proliferation and making a chimaeric molecule. The coiled coil chimaeric molecule comprises a domain belonging to a matrix protein family, transcription factor family, growth factor family or secretory protein family. The coiled coil domain is from cartilage matrix protein (CMP) or cartilage oligomeric matrix protein (COPM). The receptor-binding domain binds to Tie2 or Tiel receptor. The receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -2, -3 or -4. The chimaeric molecules are useful for promoting or inhibiting a differential function and/or influencing the phenotype, such as growth, survival, contractility, migration and/or proliferation of receptor-bearing cells such as endothelial cells, haematopoietic stem cells and endothelial precursor cells. The present sequence represents the fibrinogen-like domain of Ang-1 with a protryptsin leader.

Sequence 261 AA;

Query Match 100.0%; Score 106; DB 8; Length 261;  
Best Local Similarity 100.0%; Pred. No. 1.4e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTPKEGVLLKGKGRKEEKPF 20

Db 139 LCTPKEGVLLKGKGRKEEKPF 158

RESULT 6  
ADD23638  
ID ADD23638 standard protein; 298 AA.  
XX ADI23638;  
AC AC\_7  
XX DT 22-APR-2004 (first entry)  
XX DB Yeast Gcn4 coiled-coil domain/Human Ang-1 cDNA.  
XX

KW Human; Ang-1; fibrinogen-like domain; Protryptsin signal;  
angiopoietin; coiled-coil domain; cell growth; proliferation;  
matrix protein; transcription factor; growth factor; secretory protein;  
cartilage matrix protein; CMP; cartilage oligomeric matrix protein;  
Tie2 receptor; Tiel receptor; endothelial cell; haematopoietic stem cell;  
endothelial precursor cell; yeast.  
OS Homo sapiens.  
OS Saccharomyces cerevisiae.  
OS Chimeric.  
XX US2003220476-A1.  
XX 27-NOV-2003.  
XX 18-OCT-2002; 2002US-00273180.  
XX 21-MAY-2002; 2002US-0382541D.  
XX (KOHG/) KOH G Y.  
XX WPI; 2004-010889/01.  
DR N-PSDB; ADI23637.

XX New coiled coil chimeric molecule comprising a coiled-coil domain linked to either a receptor binding domain of ligand or ligand binding domain of a receptor, useful for inhibiting or promoting differential function.  
XX Example 5; SEQ ID NO 4; 38pp; English.  
XX

CC comprising the nucleic acid, a host cell comprising the vector, a soluble biologically active multimer comprising the coiled coil chimeric molecule, promoting cell growth or proliferation, decreasing or inhibiting ligand activity or cell proliferation and making a chimaeric molecule. The coiled coil chimaeric molecule comprises a domain belonging to a matrix protein family, transcription factor family, growth factor family or secretory protein family. The coiled coil domain is from cartilage matrix protein (CMP) or cartilage oligomeric matrix protein (COPM). The receptor-binding domain binds to Tie2 or Tiel receptor. The receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -2, -3 or -4. The chimaeric molecules are useful for promoting or inhibiting a differential function and/or influencing the phenotype, such as growth, survival, contractility, migration and/or proliferation of receptor-bearing cells such as endothelial cells, haematopoietic stem cells and endothelial precursor cells. The present sequence represents the fibrinogen-like domain of Ang-1 in a chimaeric protein with a coiled-coil domain.  
XX  
SQ Sequence 298 AA;  
XX  
Query Match 100.0%; Score 106; DB 8; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1.6e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTPKEGVLLKGKGRKEEKPF 20  
Db 64 LCTPKEGVLLKGKGRKEEKPF 83

RESULT 7  
ADD23640  
ID ADD23640 standard; protein; 310 AA.  
XX  
AC AC\_7  
XX DT 22-APR-2004 (first entry)  
XX DB Human CMP coiled-coil domain/Ang-1.  
XX Human; Ang-1; fibrinogen-like domain; Protryptsin signal;  
angiopoietin; coiled-coil domain; cell growth; proliferation;  
matrix protein; transcription factor; growth factor; secretory protein;  
cartilage matrix protein; CMP; cartilage oligomeric matrix protein;  
Tie2 receptor; Tiel receptor; endothelial cell; haematopoietic stem cell;  
endothelial precursor cell.  
XX Homo sapiens.  
OS Synthetic.  
XX US2003220476-A1.  
XX 27-NOV-2003.  
XX 18-OCT-2002; 2002US-00273180.  
XX 21-MAY-2002; 2002US-0382541P.  
XX (KOHG/) KOH G Y.  
XX WPI; 2004-010889/01.  
DR N-PSDB; ADI23639.

XX New coiled coil chimeric molecule comprising a coiled-coil domain linked to either a receptor binding domain of ligand or ligand binding domain of a receptor, useful for inhibiting or promoting differential function.  
XX Example 6; SEQ ID NO 6; 38pp; English.

CC The invention relates to a coiled coil chimaeric molecule comprising a  
 CC coiled-coil domain linked to either a receptor binding domain of a ligand  
 CC or ligand binding domain of a receptor, which forms a biologically active  
 CC multimer, and where the chimaeric molecule in its non-multimeric form is  
 CC not biologically active. Also included are an isolated nucleic acid  
 CC encoding the coiled coil chimaeric molecule, an expression vector  
 CC comprising the nucleic acid, a host cell comprising the vector, a soluble  
 CC biologically active multimer comprising the coiled coil chimaeric  
 CC molecule, promoting cell growth or proliferation, decreasing or  
 CC inhibiting ligand activity or cell proliferation, and making a chimaeric  
 CC molecule. The coiled coil chimaeric molecule comprises a domain belonging  
 CC to a matrix protein family, transcription factor family, growth factor  
 CC family or secretory protein family. The coiled coil domain is from  
 CC cartilage matrix protein (COMP) or cartilage oligomeric matrix protein  
 CC (COMP). The receptor-binding domain binds to Tie2 or Tie1 receptor. The  
 CC receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -  
 CC 2, -3 or -4. The chimaeric molecules are useful for promoting or  
 CC inhibiting a differential function and/or influencing the phenotype, such  
 CC as growth, survival, contraction, migration and/or proliferation of  
 CC receptor-bearing cells, such as endothelial cells, haematopoietic stem  
 CC cells and endothelial precursor cells. The present sequence represents  
 CC the fibrinogen-like domain of Ang-1 in a chimaeric protein with a coiled-  
 CC coil domain.  
 XX Sequence 310 AA;

Query Match 100.0%; Score 106; DB 8; Length 310;

Best Local Similarity 100.0%; Pred. No. 1.7e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTREGVLLKGKREBKF 20  
 Db 76 LCTREGVLLKGKREBKF 95

RESULT 8  
 ID AD123642 standard; protein; 312 AA.  
 XX AC AD123642;  
 XX DT 22-APR-2004 (first entry)

DE Human COMP coiled-coil domain/Ang-1.

XX Human; Ang-1; fibrinogen-like domain; Preprotryptin signal;  
 KW angiopoietin1; coiled-coil domain; cell growth; proliferation;  
 KW matrix protein; transcription factor; growth factor; secretory protein;  
 KW cartilage matrix protein; COMP; cartilage oligomeric matrix protein;  
 KW Tie2 receptor; Tie1 receptor; endothelial cell; haematopoietic stem cell;  
 KW endothelial precursor cell.  
 XX Homo sapiens.  
 OS Synthetic.

XX PN US2003220476-A1.  
 XX PD 27-NOV-2003.  
 XX PF 18-OCT-2002; 2002US-00273180.  
 XX PR 21-MAY-2002; 2002US-0382541P.  
 XX PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (KOHG/ ) KOH G Y.  
 XX PI Ellis LM;  
 XX DR WPI; 2003-697465/66.

XX DR WPI; 2004-010689/01.  
 XX DR N-PSDB; AD123641.  
 XX PT New coiled coil chimeric molecule comprising a coiled-coil domain linked  
 PT to either a receptor binding domain of ligand or ligand binding domain of  
 PT a receptor, useful for inhibiting or promoting differential function.  
 XX Disclosure; Page 139-140; 157pp; English.

XX PS Example 7; SEQ ID NO 8; 38pp; English.

XX PS The invention relates to a coiled coil chimaeric molecule comprising a  
 CC coiled-coil domain linked to either a receptor binding domain of a ligand  
 CC or ligand binding domain of a receptor, which forms a biologically active  
 CC multimer, and where the chimaeric molecule in its non-multimeric form is  
 CC not biologically active. Also included are an isolated nucleic acid  
 CC encoding the coiled coil chimaeric molecule, an expression vector  
 CC comprising the nucleic acid, a host cell comprising the vector, a soluble  
 CC biologically active multimer comprising the coiled coil chimaeric  
 CC molecule, promoting cell growth or proliferation, decreasing or  
 CC inhibiting ligand activity or cell proliferation and making a chimaeric  
 CC molecule. The coiled coil chimaeric molecule comprises a domain belonging  
 CC to a matrix protein family, transcription factor family, growth factor  
 CC family or secretory protein family. The coiled coil domain is from  
 CC cartilage matrix protein (COMP) or cartilage oligomeric matrix protein  
 CC (COMP). The receptor-binding domain binds to Tie or Tie1 receptor. The  
 CC receptor-binding domain is a fibrinogen-like domain of angiopoietin-1, -  
 CC 2, -3 or -4. The chimaeric molecules are useful for promoting or  
 CC inhibiting a differential function and/or influencing the phenotype, such  
 CC as growth, survival, contraction, migration and/or proliferation of  
 CC receptor-bearing cells such as endothelial cells, haematopoietic stem  
 CC cells and endothelial precursor cells. The present sequence represents  
 CC the fibrinogen-like domain of Ang-1 in a chimaeric protein with a coiled-  
 CC coil domain.

XX Sequence 312 AA;

Query Match 100.0%; Score 106; DB 8; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTREGVLLKGKREBKF 20  
 Db 78 LCTREGVLLKGKREBKF 97

RESULT 9  
 ID AAB38503 standard; protein; 402 AA.  
 XX AC AAB38503;  
 XX DT 20-NOV-2003 (first entry)  
 XX DE Human angiopoietin-1 #4.  
 XX KW angiopoietin1; endothelium; cell proliferation; tumour; gene therapy;  
 KW human.  
 XX OS Homo sapiens.  
 XX PN WO2003068165-A2.  
 XX PD 21-AUG-2003.  
 XX PF 14-FEB-2003; 2003WO-US004555.  
 XX PR 14-FEB-2002; 2002US-0356809P.  
 XX PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX PI Ellis LM;  
 XX DR WPI; 2003-697465/66.

XX PT Stabilizing the endothelium or reducing endothelial cell proliferation  
 PT associated with a tumor comprises administering to a patient having a  
 PT tumor angiopoietin-1 polypeptide.

XX Disclosure; Page 139-140; 157pp; English.

The invention relates to a method for stabilising the endothelium or reducing endothelial cell proliferation associated with a tumour by administering Angiopoietin-1 polypeptide to a patient having tumour. The method is useful for stabilising the endothelium or reducing endothelial cell proliferation associated with a tumour. It is also useful in gene therapy. The present sequence is human angiopoietin-1. This sequence is used to illustrate the method of the invention

Sequence 402 AA;

Query Match 100.0%; Score 106; DB 7; Length 402;  
Best Local Similarity 100.0%; Pred. No. 2.2e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 LCTKREGVLLKGGRBEEKPP 20  
Db 264 LCTKREGVLLKGGRBEEKPP 283

RESULT 10  
ID AE81248 standard; protein; 402 AA.  
XX AE81248;  
XX DT 25-AUG-2005 (first entry)  
XX DB Human angiopoietin 1 (ANGPT1), transcript variant 2 protein.  
XX KW screening; obesity; nutritional disorder; anorectic; angiopoietin 1;  
KW ANGPT1; transcript variant.  
XX HOMO SAPIENS.  
XX PN US2005136465-A1.  
XX PD 23-JUN-2005.  
XX PR 22-DEC-2004; 2004US-00019829.  
XX PR 22-DEC-2003; 2003EP-00104902.  
XX PA (CLERC / CLERC R G.  
(DUCH / DUCHATEAU-NGUYEN G.  
(GARD / GARDES C.  
(MIZR / MIZRAHI J.  
(OSTE / OSTENSON C.  
XX PI Clerc RG, Duchateau-Nguyen G, Gardes C, Mizrahi J, Ostenson C;  
XX DR 2005-457507/46.  
XX N-PSDB; AE81187.

Screening test compounds that reduce and/or prevent obesity involves contacting cell expressing gene from alpha-two-glycoprotein.

Claim 20; SEQ ID NO 115; 21DP; English.  
XX DR 2005-457507/46.  
XX N-PSDB; AE81187.

The invention relates to a novel method for screening for test compounds that reduce and/or prevent obesity. The method comprises contacting a cell expressing a gene selected from SEQ ID NO. 1-12 or 25-85, with a compound. The method of the invention demonstrates anorectic applications and may be useful for screening for compounds that reduce and/or prevent obesity. The current sequence is that of the human angiopoietin 1 (ANGPT1), transcript variant 2 protein of the invention. The sequence listing for the specification can be located via the USPRO web-site.

Sequence 402 AA;

Query Match 100.0%; Score 106; DB 9; Length 402;  
Best Local Similarity 100.0%; Pred. No. 2.2e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 456 AA;

Qy 1 LCTKREGVLLKGGRBEEKPP 20  
Db 264 LCTKREGVLLKGGRBEEKPP 283

RESULT 11  
ID ADS13776 standard; protein; 456 AA.  
XX AC ADS13776;  
XX DT 02-DEC-2004 (first entry)  
XX DB Mouse Ang-1 protein non-ECM-binding fragment.  
XX KW Ang-1; extracellular matrix; ECM; angiopoietin; cytosstatic; vasotropic;  
KW antidiabetic; antiarthritic; cerebroprotective; antiangiogenic;  
KW gene therapy; mouse.  
XX OS Mus sp.  
XX PN WO2004076650-A2.  
XX PD 10-SEP-2004.  
XX PF 27-FEB-2004; 2004WO-US006101.  
XX PR 27-FEB-2003; 2003US-0450582P.  
XX PA (UYPE-) UNIV PENNSYLVANIA.  
XX PI Yu Q;  
XX DR WPI; 2004-653413/63.  
XX N-PSDB; ADS13794.  
XX PT New pharmaceutical composition comprises a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or ischemia.  
XX PS Claim 5; SEQ ID NO 8; 114pp; English.  
XX The invention relates to a pharmaceutical composition comprising a pharmaceutical carrier and an amount of an extracellular matrix (ECM)-binding fragment of angiopoietin (Ang)-1 protein or a mutant Ang-1. Also provided are methods of treating an individual having coronary artery disease, vascular disease or a condition involving ischaemia; of promoting angiogenesis; of endothelial survival and maintaining vascular integrity in an individual; of treating an individual suspected of having a disease related to lack of blood vessels to effectively promote angiogenesis in the patients with the diseases related to lack of blood vessels such as ischaemia in hearts and limbs; to reduce stroke, heart attack, blood vessel blockage, haemorrhage, arterooclerosis risk by maintaining the health and integrity of blood vessels; to assist the recovery of the patients who had stroke and the angioplasty procedure by promoting the growth/survival of endothelial cells and establish endothelial monolayer and inhibit excessive inflammation, haemorrhage, and proliferation of vascular smooth muscle; to treat patients with restenosis by inhibiting re-closure of blood vessels after inserting stents into blood vessels; to make stable and functional artificial blood vessels comprising using the composition above; of identifying compounds that modulates binding of Ang-1 to ECM; of treating an individual suspected of being at risk of diabetes and/or arthritis in an individual developing diabetes or arthritis. The pharmaceutical composition is useful for treating diseases and disorders, e.g. cancer, coronary artery disease, vascular disease, ischaemia, restenosis, diabetes, stroke, angiogenesis, or arthritis. The present sequence represents a non-ECM-binding fragment of Ang-1 protein.



XX AAR94603;  
 AC ID AAW01409 standard; protein; 498 AA.  
 XX XX  
 XX DT 28-OCT-1996 (first entry)  
 XX DE Human TIE-2 ligand 1 derived from lambda-gt10 clone.  
 XX DT 11-FEB-1997 (first entry)  
 XX Human TIE-2 ligand 1 (lambda-gt10 clone product).  
 KW TIE-2 ligand 1; tyrosine kinase with Ig and EGF homology domain;  
 KW receptor; agonist; neovascularisation; wound healing; ischaemia;  
 KW leukopenia; thrombocytopenia; anaemia; angiogenesis; tumour;  
 KW atherosclerosis; inflammation; diagnosis; therapy.  
 OS Homo sapiens.  
 XX  
 PH OS Homo sapiens.  
 FT Location/Qualifiers  
 269  
 /note= "extra Gly residue not present in TIE-2 ligand 1  
 derived from T98G clone (see AAT14649 and AAR94604)"  
 XX  
 PN W09611269-A2.  
 XX  
 PD 18-APR-1996.  
 XX 06-OCT-1995;  
 PP 95WO-US012935.  
 XX  
 PR 07-OCT-1994;  
 PR 94US-00319932.  
 PR 27-OCT-1994;  
 PR 94US-00330261.  
 PR 02-DEC-1994;  
 PR 94US-00344922.  
 PR 09-DEC-1994;  
 PR 94US-00353503.  
 PR 17-JAN-1995;  
 PR 95US-00373507.  
 PR 06-APR-1995;  
 PR 95US-00418595.  
 XX  
 PA (REGE-)  
 PA (REGE-)  
 PA (REGENERON PHARM INC.).  
 PI Davis S, Bruno J, Goldfarb M, Aldrich TH, Maisonpierre PC;  
 PI Radziejewski C, Jones PF, Yancopoulos GD;  
 XX WPI: 1996-209850/21.  
 DR N-PSDB; AAT14648.  
 XX  
 PT Nucleic acid encoding TIE-2 ligand and related vectors - useful in  
 PT diagnosis and treatment of neovascularisation, tumours, etc., or to  
 PT promote wound healing, etc.  
 XX  
 PS Claim 2: Fig 4; B4pp; English.  
 XX AAR94603 is a recombinant human TIE-2 (hTIE-2) ligand 1 derived from a  
 CC lambda-gt10 clone. The ligand has an extra Gly residue (aa 269) as  
 CC compared to the hTIE-2 ligand from a T98G clone (see AAT14649 and  
 CC AAR94604). hTIE-2 ligand DNAs of the invention are recombinant versions  
 CC of the native ligand coding sequences and may be used to produce the  
 CC ligands at a high yield. Antibodies and receptor bodies that bind to TIE-  
 CC 2 ligands may be used to inhibit angiogenesis and neovascularisation.  
 CC themselves are useful to promote neovascularisation and wound healing  
 CC e.g. for treatment of ischaemia. TIE-2 ligands are also useful to treat  
 CC thromboembolic disease, atherosclerosis, inflammation and diabetes.  
 CC Ligand bodies contg. TIE-2 ligands may also be useful for the delivery  
 CC and targeting of growth factors, toxins etc. to sites where their  
 CC presence is advantageous  
 XX Sequence 498 AA;  
 SQ  
 Query Match 100.0%; Score 106; DB 2; Length 498;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LCTKEGVLLKGKGRREEKPF 20  
 Db 264 LCTKEGVLLKGKGRREEKPF 283  
 Search completed: May 11, 2006, 11:33:14  
 Job time : 185 secs

Copyright (c) 1993 - 2006 Biocceleration Ltd.	GenCore version 5.1.8	30	43	40.6	1792	2	T08878
OM protein - protein search, using sw model		31	42.5	40.1	71	2	C82807
Run on:	May 11, 2006, 11:33:31 ; Search time 38 Seconds (without alignments)	32	42.5	40.1	204	2	B64507
Title:	US-10-789-222-1	33	42.5	40.1			F71091
Perfect score:	106	34	42	39.6	134	2	S39046
Sequence:	1 LCTKEGVLLKGGRBEEKPF 20	35	42	39.6	137	2	156498
Scoring table:	BLOSUM62	36	42	39.6	140	2	A49659
Gapop 10.0 , Gapext 0.5		37	42	39.6	149	2	B43959
Searched:	283416 seqs, 96216763 residues	38	42	39.6	187	2	S10721
Total number of hits satisfying chosen parameters:	283416	39	42	39.6	188	1	XKPO0C
Minimum DB seq length: 0		40	42	39.6	220	1	XKPO0D
Maximum DB seq length: 2000000000		41	42	39.6	220	2	S52656
Post-processing: Minimum Match 0%		42	42	39.6	220	2	S24186
Maximum Match 100%		43	42	39.6	221	2	T07411
Database :	PIR_80.4*	44	42	39.6	221	2	T07413
	1: pi1:*	45	42	39.6	221	2	JQ2246
	2: pi2:*						
	3: pi3:*						
	4: pi4:*						

## ALIGNMENTS

RESULT 1							
B86599	metal transport P-type ATPase [imported] - <i>Chlamydophila pneumoniae</i> (strain J138)	Query Match	46.2%	Score 49;	DB 2;	Length 658;	
C;Species: <i>Chlamydophila pneumoniae</i> , <i>Chlamydia pneumoniae</i>	Best Local Similarity 81.8%	Prd. No. 16;					
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004	Matches 9;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;		
C;Accession: B86599	Qy	2 CTREGVLLKG 12					
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Shiba, T.; Ito, A;Title: Comparison of whole genome sequences of <i>chlamydia pneumoniae</i> J138.	Db	331 CAKHFGLLKGG 341					
A;Reference number: A86491; PMID:20330349; PMID:10871362							
A;Accession: B86599							
A;Status: preliminary							
A;Molecule type: DNA							
A;Residues: 1-658 < STO>							
A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:BA000008; NID:98979242; PII: F478-620							
A;Experimental source: strain J138							
C;Genetics:							
A;Gene: zntA							
C;Superfamily: <i>Enterococcus</i> copper-transporting ATPase copB; ATPase nucleotide-binding d:							
RESULT 2							
B86599	metal transport P-type ATPase - <i>Chlamydophila pneumoniae</i> (strain CWL029)	Query Match	46.2%	Score 49;	DB 2;	Length 658;	
C;Species: <i>Chlamydophila pneumoniae</i> , <i>Chlamydia pneumoniae</i>	Best Local Similarity 81.8%	Prd. No. 16;					
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004	Matches 9;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;		
C;Accession: D72026	Qy	2 CTREGVLLKG 12					
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999	Db	331 CAKHFGLLKGG 341					
A;Title: Comparative genomes of <i>Clamydia pneumoniae</i> and <i>C. trachomatis</i> .							
A;Reference number: A72000; PMID:99206606; PMID:10132388							
A;Accession: D72026							
A;Status: preliminary							
A;Molecule type: DNA							
A;Residues: 1-658 < ARN>							
A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:AE001667; GB:AE001363; NID: F478-620							
A;Experimental source: strain CWL029							
C;Genetics:							
A;Gene: zntA							
C;Superfamily: <i>Enterococcus</i> copper-transporting ATPase copB; ATPase nucleotide-binding d:							
B86599	5-enoxybutyrylshikimic acid finger protein	Query Match	46.2%	Score 49;	DB 2;	Length 658;	
C;Species: <i>Enterococcus</i> copper-transporting ATPase copB; ATPase nucleotide-binding d:	Best Local Similarity 81.8%	Prd. No. 16;					
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004	Matches 9;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;		
C;Accession: D72026	Qy	2 CTREGVLLKG 12					
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999	Db	331 CAKHFGLLKGG 341					
A;Title: Comparative genomes of <i>Clamydia pneumoniae</i> and <i>C. trachomatis</i> .							
A;Reference number: A72000; PMID:99206606; PMID:10132388							
A;Accession: D72026							
A;Status: preliminary							
A;Molecule type: DNA							
A;Residues: 1-658 < ARN>							
A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:AE001667; GB:AE001363; NID: F478-620							
A;Experimental source: strain CWL029							
C;Genetics:							
A;Gene: zntA							
C;Superfamily: <i>Enterococcus</i> copper-transporting ATPase copB; ATPase nucleotide-binding d:							
B86599	legumin-like protein	Query Match	46.2%	Score 49;	DB 2;	Length 658;	
C;Species: <i>Enterococcus</i> copper-transporting ATPase copB; ATPase nucleotide-binding d:	Best Local Similarity 81.8%	Prd. No. 16;					
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004	Matches 9;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;		
C;Accession: D72026	Qy	2 CTREGVLLKG 12					
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999	Db	331 CAKHFGLLKGG 341					
A;Title: Comparative genomes of <i>Clamydia pneumoniae</i> and <i>C. trachomatis</i> .							
A;Reference number: A72000; PMID:99206606; PMID:10132388							
A;Accession: D72026							
A;Status: preliminary							
A;Molecule type: DNA							
A;Residues: 1-658 < ARN>							
A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:AE001667; GB:AE001363; NID: F478-620							
A;Experimental source: strain CWL029							
C;Genetics:							
A;Gene: zntA							
C;Superfamily: <i>Enterococcus</i> copper-transporting ATPase copB; ATPase nucleotide-binding d:							
B86599	nitrate/nitrite reductase	Query Match	46.2%	Score 49;	DB 2;	Length 658;	
C;Species: <i>Enterococcus</i> copper-transporting ATPase copB; ATPase nucleotide-binding d:	Best Local Similarity 81.8%	Prd. No. 16;					
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004	Matches 9;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;		
C;Accession: D72026	Qy	2 CTREGVLLKG 12					
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999	Db	331 CAKHFGLLKGG 341					
A;Title: Comparative genomes of <i>Clamydia pneumoniae</i> and <i>C. trachomatis</i> .							
A;Reference number: A72000; PMID:99206606; PMID:10132388							
A;Accession: D72026							
A;Status: preliminary							
A;Molecule type: DNA							
A;Residues: 1-658 < ARN>							
A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:AE001667; GB:AE001363; NID: F478-620							
A;Experimental source: strain CWL029							
C;Genetics:							
A;Gene: zntA							
C;Superfamily: <i>Enterococcus</i> copper-transporting ATPase copB; ATPase nucleotide-binding d:							
B86599	nitrate/nitrite reductase	Query Match	46.2%	Score 49;	DB 2;	Length 658;	
C;Species: <i>Enterococcus</i> copper-transporting ATPase copB; ATPase nucleotide-binding d:	Best Local Similarity 81.8%	Prd. No. 16;					
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004	Matches 9;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;		
C;Accession: D72026	Qy	2 CTREGVLLKG 12					
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999	Db	331 CAKHFGLLKGG 341					
A;Title: Comparative genomes of <i>Clamydia pneumoniae</i> and <i>C. trachomatis</i> .							
A;Reference number: A72000; PMID:99206606; PMID:10132388							
A;Accession: D72026							
A;Status: preliminary							
A;Molecule type: DNA							
A;Residues: 1-658 < ARN>							
A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:AE001667; GB:AE001363; NID: F478-620							
A;Experimental source: strain CWL029							
C;Genetics:							
A;Gene: zntA							
C;Superfamily: <i>Enterococcus</i> copper-transporting ATPase copB; ATPase nucleotide-binding d:							
B86599	nitrate/nitrite reductase	Query Match	46.2%	Score 49;	DB 2;	Length 658;	
C;Species: <i>Enterococcus</i> copper-transporting ATPase copB; ATPase nucleotide-binding d:	Best Local Similarity 81.8%	Prd. No. 16;					
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004	Matches 9;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;		
C;Accession: D72026	Qy	2 CTREGVLLKG 12					
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999	Db	331 CAKHFGLLKGG 341					
A;Title: Comparative genomes of <i>Clamydia pneumoniae</i> and <i>C. trachomatis</i> .							
A;Reference number: A72000; PMID:99206606; PMID:10132388							
A;Accession: D72026							
A;Status: preliminary							
A;Molecule type: DNA							
A;Residues: 1-658 < ARN>							
A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:AE001667; GB:AE001363; NID: F478-620							
A;Experimental source: strain CWL029							
C;Genetics:							
A;Gene: zntA							
C;Superfamily: <i>Enterococcus</i> copper-transporting ATPase copB; ATPase nucleotide-binding d:							
B86599	nitrate/nitrite reductase	Query Match	46.2%	Score 49;	DB 2;	Length 658;	
C;Species: <i>Enterococcus</i> copper-transporting ATPase copB; ATPase nucleotide-binding d:	Best Local Similarity 81.8%	Prd. No. 16;					
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004	Matches 9;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;		
C;Accession: D72026	Qy	2 CTREGVLLKG 12					
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999	Db	331 CAKHFGLLKGG 341					
A;Title: Comparative genomes of <i>Clamydia pneumoniae</i> and <i>C. trachomatis</i> .							
A;Reference number: A72000; PMID:99206606; PMID:10132388							
A;Accession: D72026							
A;Status: preliminary							
A;Molecule type: DNA							
A;Residues: 1-658 < ARN>							
A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:AE001667; GB:AE001363; NID: F478-620							
A;Experimental source: strain CWL029							
C;Genetics:							
A;Gene: zntA							
C;Superfamily: <i>Enterococcus</i> copper-transporting ATPase copB; ATPase nucleotide-binding d:							
B86599	nitrate/nitrite reductase	Query Match	46.2%	Score 49;	DB 2;	Length 658;	
C;Species: <i>Enterococcus</i> copper-transporting ATPase copB; ATPase nucleotide-binding d:	Best Local Similarity 81.8%	Prd. No. 16;					
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004	Matches 9;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;		
C;Accession: D72026	Qy	2 CTREGVLLKG 12					
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999	Db	331 CAKHFGLLKGG 341					
A;Title: Comparative genomes of <i>Clamydia pneumoniae</i> and <i>C. trachomatis</i> .							
A;Reference number: A72000; PMID:99206606; PMID:10132388							
A;Accession: D72026							
A;Status: preliminary							
A;Molecule type: DNA							
A;Residues: 1-658 < ARN>							
A;Cross-references: UNIPROT:Q9Z738; UNIPARC:UPI00000D404D; GB:AE001667; GB:AE001363; NID: F478-620							
A;Experimental source: strain CWL029							
C;Genetics:							
A;Gene: zntA							
C;Superfamily:							

RESULT 3									
81742									
Annotations-translating ATPase, E1-E2 family TC0100 [imported] - Chlamydia muridarum (strain									
Species: Chlamydia muridarum, Chlamydia trachomatis MoPn									
ID: AE002277; UNIPARC:UPI00000577C9; GB:AE002160; NID									
Accession: A81742									
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.; Nucleic Acids Res. 28, 1397-1406, 2000									
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.									
A; Reference number: A81500; MUID:20150255; PMID:10684935									
A; Accession: CB1515									
A; Status: preliminary									
A; Molecule type: DNA									
A; Residues: 1-683 <RE>									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									
A; Cross-references: UNIPROT:Q9KU00; UNIPARC:UPI00000577C9; GB:AE002277; NID									
A; Experimental source: strain AR39, HL cells									

A:Experimental source: tadpole, brain
A:Note: this protein has motifs homologous to complement components C1r and C1s and to C:Comment: This protein is a neuronal cell surface molecule involved in the neuronal recognition of the C5a peptide.
C:Superfamily: Xenopus A5 antigen; C1r/C1s repeat homology; discoidin I amino-terminal homology
C:Keywords: duplication; glycoprotein; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SG>
F:22-928/Domain: A5 antigen #status predicted <SGA>
F:27-138/Domain: C1r/C1s repeat homology <C1R1>
F:147-362/Domain: C1r/C1s repeat homology <C1R2>
F:274-324/Domain: discoidin I amino-terminal homology <DN1>
F:430-594/Domain: discoidin I amino-terminal homology <DN2>
F:646-812/Domain: MAM homology <MAM>
F:861-883/Domain: transmembrane #status predicted <TMM>
F:150,261-300,525,844/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 44.3%; Score 47; DB 1; Length 927;
Best Local Similarity 53.3%; Pred. No. 44;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Qy 6 GVLKGGKRBEERF 20
Db 498 GVIQGGKHKENKF 512
RESULT 8
SYHUTP
CTP synthase (EC 6.3.4.2) - human
N;Alternate names: CTP-synthetase; UTP-ammonia ligase
C:Species: Homo sapiens (man)
C:Accession: S12791 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
R:Yamauchi, M.; Yamauchi, N.; Meuth, M.
EMBO J. 9, 2095-2099, 1990
A:Title: Molecular cloning of the human CTP synthetase gene by functional complementation
A:Reference number: S12791; MUID:90291972; PMID:2113467
A:Accession: S12791
A:Molecule type: mRNA
A:Residues: 1-591 <YAM>
A:Cross-references: UNIPROT:P17812; UNIPARC:UPI000163BFD; GB:X52142; PIDN:Q36230
C:Comment: This enzyme is a glutamine amidotransferase that catalyzes the terminal reaction in the synthesis of CTP.
C:Genetics:
A:Gene: GDB:CTPS
A:Cross-references: GDB:126729; OMIM:123860
A:Map position: 1p34.3-1p34.1
C:Superfamily: CTP synthase
C:Keywords: ligase; pyrimidine nucleotide biosynthesis
Query Match 43.9%; Score 46.5%; DB 1; Length 591;
Best Local Similarity 31.4%; Pred. No. 35;
Matches 11; Conservative 4; Mismatches 5; Indels 15; Gaps 1;
Qy 1 LCTPKEGVNLKGG-----KREEEERKF 20
Db 361 LCSRHNGLVLPGGFVRGTEGKIQIAIWARNQKRF 395
RESULT 9
S01371
myosin heavy chain, cardiac and skeletal muscle - eastern newt (fragment)
C:Species: Notophthalmid viridescens, Triturus viridescens (eastern newt)
C:Accession: 30-Sep-1989 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: S01371; S67907
R:Casimir, C.M.; Gates, P.B.; Ross-Macdonald, P.B.; Jackson, J.F.; Patient, R.K.; Brocke, J. Mol. Biol. 202, 287-296, 1988
A:Title: Structure and expression of a new cardio-skeletal myosin gene. Implications for the evolution of myosin heavy chains.
A:Reference number: S01371; MUID:89011957; PMID:2459393
A:Accession: S01371
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-171 <CAs>
A:Cross-references: UNIPROT:Q7LZB4; UNIPARC:UPI000177608
A:Accession: S67907
A:Note: the sequence from fig. 7 is inconsistent with that from fig. 5 in having 64-116

S15675  
Globulin-2 precursor - maize  
C;Species: Zea mays (maize)  
C;Date: 18-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S15675  
R;Wallace, N. H.; Kriz, A. L.  
Plant Physiol., 95, 971-975, 1991  
A;Title: Nucleotide sequence of a cDNA clone corresponding to the maize globulin-2 gene.  
A;Reference number: S15675  
A;Accession: S15675  
A;Status: Preliminary  
A;Molecule type: mRNA  
A;Residues: 1-450 <WAT>  
A;Cross-references: UNIPROT:Q7M128; UNIPARC:UPI0000177E41

Query Match 42.5%; Score 45; DB 2; Length 450;  
Best Local Similarity 68.8%; Pred. No. 45;  
Matches 11; Conservative 1; Mismatches 0; Indels 4; Gaps 1;  
Qy 4 KEG---VILKGKRE 15  
Db 95 KEGERGVIVLRRGGRE 110

RESULT 13  
T29766  
hypothetical protein ZC581.5 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T29766  
R;Waterston, R.; Gattung, S.; Le, T.T.  
Submitted to the EMBL Data Library, May 1997  
A;Description: The sequence of C. elegans cosmid ZC581.  
A;Reference number: Z22682  
A;Accession: T29766  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-97 <WAT>  
A;Cross-references: UNIPARC:UPI000017BCE4; EMBL:AF003134; PIDN:AA554143.1; GSPDB:GN00019  
A;Experimental source: strain Bristol N2; clone ZC581  
C;Genetics:  
A;Gene: CESP\_ZC581.5  
A;Map position: 1  
A;Introns: 74/1

Query Match 41.5%; Score 44; DB 2; Length 97;  
Best Local Similarity 53.8%; Pred. No. 15;  
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
Qy 5 EGVILKGKRE 17  
Db 31 ERINMKGGNEED 43

RESULT 14  
T48751  
hypothetical protein 8D4.250 [imported] - Neurospora crassa  
C;Species: Neurospora crassa  
C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 19-May-2000  
C;Accession: T48751  
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Hartmann, B.; Holland, R.; Nyakatura, A.; Submitted to the Protein Sequence Database, April 2000  
A;Reference number: 224541  
A;Accession: T48751  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-141 <SCH>  
A;Cross-references: UNIPARC:UPI0000179478; EMBL:AL3551819; GSPDB:GN00112; NCSP:8D4.250  
A;Experimental source: cosmid contig 8D4; strain 74  
C;Genetics:  
A;Gene: NCSP:8D4.250  
A;Map position: 2

S15675  
C;Superfamily: Neurospora crassa hypothetical protein 8D4.250  
Query Match 41.5%; Score 44; DB 2; Length 141;  
Best Local Similarity 64.3%; Pred. No. 21;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
Qy 3 TKEGVILKGKRE 16  
Db 74 TNGKULSGGKED 87

RESULT 15  
T20508  
hypothetical protein F02E9.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T20508  
R;Gray, I.  
submitted to the EMBL Data Library, November 1996  
A;Reference number: 219285  
A;Accession: T20508  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Cross-references: UNIPROT:001314; UNIPARC:UPI0000074F98; EMBL:Z81494; PIDN:CA04047.1;  
A;Experimental source: clone F02E9  
C;Genetics:  
A;Gene: CESP:F02E9.1  
A;Map position: 1  
A;Introns: 29/2; 52/2; 80/3; 131/3  
Query Match 41.5%; Score 44; DB 2; Length 154;  
Best Local Similarity 60.0%; Pred. No. 23;  
Matches 12; Conservative 1; Mismatches 5; Indels 2; Gaps 1;  
Qy 1 LCTKKG--VLLKGKREBEK 18  
Db 53 LDTPKNGKPVLLKNSNEEBK 72

Search completed: May 11, 2006, 11:37:58  
Job time : 39 secs



Yancopoulos G.D.; "Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by secretion-trap expression cloning.", *Cell* 87:1161-1169(1996).

[2] NUCLEOTIDE SEQUENCE, AND VARIANT GLY-269 DEL.  
Nakatsukasa M., Komai K., Shiozawa S.; "Human angiopoietin-1 mRNA variant form.", Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

[3] NUCLEOTIDE SEQUENCE, AND VARIANT GLY-269 DEL.  
Shan Z.X., Yu X.Y., Lin Q.Y., Fu Y.H., Tan H.H., Zheng M., Lin S.G.; "Human angiopoietin-1 mRNA variant forms.", Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

[4] NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].  
TISSUE[Bone marrow;  
MEDLINE#9051036; PubMed:7584026;  
Nomura N., Miyajima N., Suzuki T., Tanaka A., Kawarabayasi Y.,  
Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;  
"Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1.", *Cell* 71:27-35(1993).  
DNA Res. 1:27-35(1994).

SEQUENCE REVISION. PubMED=12168854;  
EDDLINE=22158633; EDDLINE=22158633; PubMed=12168854;  
Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;  
"Construction of expression-ready cDNA clones for KIAA genes: manual  
curatration of 330 KIAA cDNA clones";  
DNA Res. 9:99-106 (2002).  
- FUNCTION: Binds and activates TIE2 receptor by inducing its  
tyrosine phosphorylation. Implicated in endothelial developmental  
processes later and distinct from that of VEGFR. Appears to play a  
crucial role in mediating reciprocal interactions between the  
endothelial and surrounding matrix and mesenchyme. Mediates blood  
vessel maturation/stability. It may play an important role in the

- heart early development.
- SUBCELLULAR LOCATION: Secreted.
- PTM: Glycosylated.
- MISCELLANEOUS: It may have a potential therapeutic utility since it can be used for specifically targeting tumor vasculature or for promoting angiogenic processes in certain organs such as an ischemic heart.
- SIMILARITY: Contains 1 fibrinogen C-terminal domain.

This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

U83508; AAB50557.1; - ; MERA.

EMBL; AB084454; BAB91325.1; -; mRNA.  
EMBL; AY121504; AAM81745.1; -; mRNA.

AY124380; AAM92271.1; -; mRNA.  
D13628; BAA02793.2; ALT INIT; tRNA.

ISSP; P02671; IFZD.  
research; ENSC0000015499; Homo sapiens

CHGNC; HGNC: 484; ANGPT1.

-Invnr: HIX00007720; -; IIN: 601667; -;

90; GO:0005102; F: receptor binding; TAS.

nterPro; IPR002181; Fibrinogen C.  
Defeat: DE00142; Fibrinogen C. 1

Lam/ FEB011 / FIBROGEN\_C; 1.  
SMART; SMO0186; FBG; 1.

PROSITE; PS00514; FIBRINAG C DOMAIN; 1. Angiogenesis; Coiled coil; Developmental protein; Differentiation;

glycoprotein; Polymorphism; Signal. 15 Potential.

FT	DOMAIN	284	498	Fibrinogen C-terminal.
FT	COILED	81	119	Potential.
FT	COILED	153	261	Potential.
FT	CARBOHYD	92	92	N-Linked (GICNAC. . .) (Potential).
FT	CARBOHYD	122	122	N-Linked (GICNAC. . .) (Potential).
FT	CARBOHYD	122	154	N-Linked (GICNAC. . .) (Potential).
FT	CARBOHYD	243	243	N-Linked (GICNAC. . .) (Potential).
FT	CARBOHYD	295	295	N-Linked (GICNAC. . .) (Potential).
FT	DISULFID	285	315	By similarity.
FT	DISULFID	439	452	By similarity.
FT	VARIANT	269	269	Missing (in cell line T98G; may be due to exon skipping).
FT				/FTid=VAR_005940.
SQ	SEQUENCE	498 AA;	57513 MW;	5D5FA63AEP6BEE920 CRC64;
Query Match		100.0%;	Score 106;	DB 1;
Best Local Similarity		100.0%;	Pred. No. 1.8e-07;	Length 498;
Matches	20;	Conservative	0;	Mismatches 0;
Indels	0;			GC
Qy		1 LCTKEGVLLKGGRREEEKPF 20		
Db		264 LCTKEGVLLKGGRREEEKPF 283		
<b>RESULT 3</b>				
ANGPT1_MOUSE STANDARD; PRT; 498 AA.				
AC	008538;	AC008538;	Rel. 40; Created)	
DT	16-OCT-2001	16-OCT-2001 (Rel. 40; Last sequence update)		
DT	16-OCT-2001	16-OCT-2001 (Rel. 40; Last sequence update)		
DT	10-MAY-2005	10-MAY-2005 (Rel. 47; Last annotation update)		
DE	Angiopoietin-1 precursor (ANG-1).			
GN	Name=Angpt1; Synonyms=Angpt1;			
OS	Mus musculus (Mouse).			
OC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Eutheriontognires; Glires; Rodentia; Sciurognathia;			
OC	Urodeles; Muroidea; Murinae; Mus.			
RN	[1] NCBI_TaxID=10090;			
RP	NUCLEOTIDE SEQUENCE.			
RX	Medline:97134663; PubMed:8980223; DOI=10.1016/S0092-8674(00)81812-6			
RA	Davis S., Aldrich T.H., Jones P.P., Acheson A., Compton D.L., Jaini			
RA	Ryan T.E., Bruno J., Radziejewski C., Maisonneuve P.C., Yancopoulos G.D.,			
RA	"Isolation of angiopoietin-1, a ligand for the TIE2 receptor, by RT secretion-trap expression cloning.";			
RL	Cell 87:1161-1169 (1996).			
CC	-1- FUNCTION: Binds and activates TIE2 receptor by inducing its tyrosine phosphorylation. Implicated in endothelial development.			
CC	processes later and distinct from that of VEGF. Appears to play a crucial role in mediating reciprocal interactions between the endothelium and surrounding matrix and mesenchyme. Mediates blood vessel maturation/stability. It may play an important role in heart early development.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- DEVELOPMENTAL STAGE: Early in development, at E9 to E11, it is found most prominently in the heart myocardium surrounding the endocardium. Later, it becomes more widely distributed, most of all in the mesenchyme surrounding developing vessels, in close association with endothelial cells.			
CC	-1- SIMILARITY: Contains 1 Fibrinogen C-terminal domain.			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on use as long as its content is in no way modified and this statement is removed.			
CC	EMBL; U83509; AAB50558.1; - ; mRNA.			
DR	HSSP; P02671; 1FZD.			
DR	Ensembl; ENSMUSG0000022309; Mus musculus.			
DR	MGI; MGI:1108449; Angpt1.			
DR	GO:0005615; C: extracellular space; TAS.			

```

DR GO:GO:0005172; P:vascular endothelial growth factor receptor. . . ; TAS.
DR GO:GO:0007432; P:endothel development; TAS.
DR GO:GO:0007165; P:transmembrane receptor protein tyrosine kin. . . ; IDA.
DR InterPro:IPR002131; Fibrinogen_C.
DR Pfam:PF00147; Fibrinogen_C; 1.
SMART:SM00185; FBC; 1.
PROSITE:PS00514; FIBRIN AG C DOMAIN; 1.
KW Angiogenesis; Coiled coil; Developmental protein; Differentiation;
Glycoprotein; Signal.
KW NUCLEOTIDE SEQUENCE.
FT SIGNAL 1 19
FT CHAIN 20 498 Angiopoietin-1.
FT DOMAIN 284 498 Fibrinogen C-terminal.
FT COILED 81 19 Potential.
FT COILED 153 261 Potential.
FT CARBOHYD 92 92 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 122 122 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 154 154 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 243 243 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 295 295 N-linked (GlcNAc. . .) (Potential).
FT DISULFID 286 315 By similarity.
FT DISULFID 439 452 By similarity.
SQ SEQUENCE 498 AA; 57505 MW; 285B4FB26D800 CRC64;
Query Match 100.0%; Score 106; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.be-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTKEGVLLKGGRKREEEKKP 20
Db 264 LCTKEGVLLKGGRKREEEKKP 283

```

```

RESULT 4
Q5YAO HUMAN HUMAN PRELIMINARY;
ID Q5YAO_HUMAN_HUMAN_PRELIMINARY; PRT; 498 AA.
AC Q5YAO_HUMAN_HUMAN_PRELIMINARY; Created.
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DT Hypothetical protein DKRZp68610222.
DB Name=DKRZp68610222;
GN Homo sapiens (Human).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=small intestine;
RA The German cDNA Consortium;
RA Bahr A., Lauher J., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Hahn M., Wiemann S. ;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX648814; CBI45984.1; -; mRNA.
KW Hypothetical protein.
SEQUENCE 498 AA; 57513 MW; 5D5FA63AEF6BE920 CRC64;

```

```

Q5YAO HUMAN HUMAN PRELIMINARY;
ID Q5YAO_HUMAN_HUMAN_PRELIMINARY; PRT; 498 AA.
AC Q5YAO_HUMAN_HUMAN_PRELIMINARY; Created.
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DB Mus musculus 2 days neonate thymus cDNA, RIKEN full-length enriched library, clone:E430016L03 product:angiopoietin, full insert sequence.
GN Name=Angpt1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]

```

```

DE Angiopoietin 1.
GN Name=Angpt1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Sheman C.M., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Hopkins R.F., Diatchenko L., Marusina K., Farmer A.A., Rubinstein G.M., Hong L.,
Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Mullahy S.J., Loquellano N.A., Peters G.J., Abramson R.D., Muller K.J., Gunaratne P.H., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Rodriguez S., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Rodriguez S., Sanchez A.,
Paley J., Helton B., Kettman M., Madan A., Shevchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Balesky R.W., Touchman J.W., Dickson M.C., Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E.,
Scheinrich A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", RT and mouse cDNA sequences.", RT
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RA Director MGC Project;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067410; AAH67410.1; -; mRNA.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:000517; P:vascular endothelial growth factor receptor. . . ; TAS.
DR GO; GO:0007492; P:endothelial growth factor receptor. . . ; TAS.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; IDA.
DR InterPro; IPR02181; Fibrinogen_C.
DR SMART; SM00186; Fibrinogen_C;
DR PFAM; PF00147; Fibrinogen_C;
DR PROSITE; PS00514; FIBRIN AG C_DOMAIN; 1.
SQ SEQUENCE 498 AA; 57513 MW; FC36F905A9879074 CRC64;

```

```

Query Match 100.0%; Score 106; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LCTKEGVLLKGGRKREEEKKP 20
Db 264 LCTKEGVLLKGGRKREEEKKP 283

```

```

RESULT 6
Q8C2K6 MOUSE PRELIMINARY;
ID Q8C2K6_MOUSE_PRELIMINARY;
AC Q8C2K6;
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DB Mus musculus 2 days neonate thymus cDNA, RIKEN full-length enriched library, clone:E430016L03 product:angiopoietin, full insert sequence.
GN Name=Angpt1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]

```

```

RESULT 5
Q6NWV7 MOUSE PRELIMINARY;
ID Q6NWV7_MOUSE_PRELIMINARY;
AC Q6NWV7;
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DB 264 LCTKEGVLLKGGRKREEEKKP 283

```

RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=JOD; TISSUE=Thymus;
RC	MEDLINE=20085660; PubMed=11217851; DOI=10.1038/35055500;
RC	RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA	Arizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA	Saito T., Oizaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA	Kadota K., Matsuda H.A., Asburyer M., Batalov S., Casavant T.,
RA	Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
RA	Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA	Schriml L.M., Staubli H., Suzuki R., Tomita M., Wagner L., Washio T.,
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA	Brown J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M.,
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombretti P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-P.,
RA	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kobayashi S.,
RA	Hayashizaki Y.;
RT	"Functional annotation of a full-length mouse cDNA collection.";
RT	Nature 409:655-690 (2001).
RN	[3]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=JOD; TISSUE=Thymus;
RC	THE PANTOM Consortium,
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;
RT	"Analysis of the mouse transcriptome based on functional annotation of
RT	60,770 full-length cDNAs.";
RT	"Normalization and subraction of cap-trapper-selected cDNAs to
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";
RT	Genome Res. 10:1617-1630 (2000).
RN	[4]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=JOD; TISSUE=Thymus.
RC	MEDLINE=20439374; PubMed=11042159; DOI=10.1101/qr.145100;
RA	Carinici P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA	Konno H., Oizaki Y., Muramatsu M., Hayashizaki Y.,
RA	"Normalization and subtraction of cap-trapper-selected cDNAs to
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";
RT	Genome Res. 10:1617-1630 (2000).
RN	[5]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=JOD; TISSUE=Thymus.
RC	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/qr.152600;
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA	Konno H., Akiyama K., Nishimi K., Katsunai T., Tashiro H., Itoh M.,
RA	Sumi N., Itoh Y., Nishimi K., Hazama M., Nishine T., Harada A.,
RA	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA	Yoneda Y., Inoue K., Togawa Y., Iwasa M., Ohara E., Watahiki M.,
RA	Oizaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA	"RIKEN integrated sequence analysis (RISA) system-384-format
RT	sequencing pipeline with 384 multicapillary sequencer.";
RT	Genome Res. 10:1757-1771 (2000).
RL	[6]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=JOD; TISSUE=Thymus;
RC	RCB: Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA	Fukuda S., Furuno M., Hanasaki T., Hara A., Hashizume W.,
RA	Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,
RA	Hori F., Imokuni K., Itoh M., Itoh Y., Kasukawa T., Katsunai T.,
RA	Katoh H., Kawai J., Kondo S., Kondo M., Koya S.,
RA	Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA	Nishi K., Nomura K., Numazaki R., Ohno M., Onsato N., Okazaki Y.,
RA	Saito R., Saitoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA	Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,



AC	Q18920;	DT	16-Oct-2001 (Rel. 40, Created)
RP	NUCLEOTIDE SEQUENCE;	DT	16-Oct-2001 (Rel. 40, Last sequence update)
RC	TISSUE-Adult spleen;	DT	16-Oct-2001 (Rel. 40, Last annotation update)
RX	PubMed:1536895;	DT	10-May-2005 (Rel. 40, Last annotation update)
RA	Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoaka S., Suga Y., Seino S., Nishimura M., Kaihori T., Hoshino K., Kitamura H., Nagase T., Ohara O., Koga H., Kozian D., Augustin H.G.;	DN	Angiopoietin-1 precursor (ANG-1) (fragment). Name=ANGPT1; Synonyms=ANG1;
RA	"Prediction of the coding sequences of mouse homologues of KIAA gene IV. The complete nucleotide sequences of 500 mouse KIAA-homologous cDNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries.";	OS	Bos taurus (Bovine). Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos. NCBI_TaxID=9913;
RL	DNA Res. 11:205-218 (2004).	RN	[1]
DR	EMBL: AK172688; BAD32446.1; - ; mRNA.	RP	NUCLEOTIDE SEQUENCE.
DR	MGT; MGI: 1084848; Angpt1.	RC	TISSUE=Ovary;
DR	GO; GO:005615: C-extracellular space; TAS.	RX	Medline=99054348; PubMed=9840613;
DR	GO; GO:1005172: F-vascular endothelial growth factor receptor. . . ; TAS.	RA	Goede V., Schmidt T., Kimmela S., Kozian D., Augustin H.G.;
DR	GO; GO:007492: P-endoderm development; TAS.	RT	"Analysis of blood vessel maturation processes during cyclic ovarian angiogenesis."
DR	GO; GO:007169: P-transmembrane receptor protein tyrosine kin. . . ; IDA.	RL	RT
DR	InterPro; IPR002181; Fibrinogen receptor.	RN	Lab. Invest. 78:1385-1394 (1998).
DR	Pfam; PF00177; Fibrinogen_C.	[2]	[2]
DR	SMART; SM00186; FBG.	RP	NUCLEOTIDE SEQUENCE OF 91-200.
DR	PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.	RC	TISSUE=Liver;
FT	NON TER 1 1	RX	Medline=98451564; PubMed=9776732;
SEQUENCE	521 AA, 60103 MW, 8E70612A570DEFA CRC64;	RA	Mandriota S.J., Pepper M.S., RA
90	Regulation of angiopoietin-2 mRNA levels in bovine microvascular endothelial cells by cytokines and hypoxia."	RT	RT
Qy	1 LCTKSEGVLKLGGRREBEEKF 20	CIR	Circ. Res. 83:852-859 (1998);
Db	288 LCTK-E-VLKGKGRREBEEKF 306	CC	-1- FUNCTION: Binds and activates TIE2 receptor by inducing its tyrosine phosphorylation. Implicated in endothelial developmental processes later and distinct from that of VEGF. Appears to play a crucial role in mediating reciprocal interactions between the endothelium and surrounding matrix and mesenchyme. Mediates blood vessel maturation/tubility. It may play an important role in the heart early development. (By similarity).
RESULT	11	CC	-1- SUBCELLULAR LOCATION: Secreted.
Q60FC1	Q60FC1 CANFA PRELIMINARY; PRT; 497 AA.	CC	-1- DEVELOPMENTAL STAGE: Found to be expressed throughout the ovarian cycle.
AC	Q60FC1;	CC	-1- SIMILARITY: Contains 1 fibrinogen C-terminal domain.
DT	25-OCT-2004 (TREMBLrel. 28, Created)	CC	-----
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)	CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)	CC	-----
DE	Angiopoietin-1.	CC	-----
GN	Name=Ang-1;	CC	-----
OS	Canis familiaris (Dog).	CC	-----
OC	Mammalia; Metazoia; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.	DR	EMBL; AF093573; AAC1672.1; - ; mRNA.
OC	NCBI_TaxID=9615;	DR	EMBL; AF032923; AAC78245.1; - ; mRNA.
RN	-----	DR	HSSP; Q9U898; 1IC9.
RP	NUCLEOTIDE SEQUENCE.	DR	Intertier; IPR02181; Fibrinogen_C.
RA	Kato Y., Asano K., Canis familiaris, Angiopoietin-1 mRNA, complete cds.";	DR	Pfam; PF00147; Fibrinogen_C.
RT	Submitted (Oct-2004) to the EMBL/GenBank/DDBJ databases.	DR	SMART; SM00186; FBG.
RL	DR	DR	PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.
DR	DR	DR	Angiogenesis; Collod coil; Developmental protein; Differentiation; Glycoprotein; Signal.
DR	DR	FT	SIGNAL 1 15
GO	GO:0007596: P-blood coagulation; IFA.	FT	CHAIN 16 >481
DR	InterPro; IPR002181; Fibrinogen_C.	FT	DOMAIN 283 >481
DR	Pfam; PF00177; Fibrinogen_C.	FT	COILED 153 261
DR	SMART; SM00186; FBG.	FT	CARBONYD 92 92
DR	PROSITE; PS00514; FIBRIN AG C DOMAIN; 1.	FT	CARBONYD 122 122
SEQUENCE	497 AA; 57415 MW; 061AFC2E03EEF081 CRC64;	FT	CARBONYD 154 154
Qy	1 LCTKSEGVLKLGGRREBEEKF 20	FT	CARBONYD 243 243
Db	284 LCTK-E-VLKGKGRREBEEKF 282	FT	CARBONYD 294 294
RESULT	12	FT	DISUPTD 285 314
ANG1	ANG1 BOVIN STANDARD; PRT; 481 AA.	FT	DISUPTD 438 451
ANG1	ANG1 BOVIN STANDARD; PRT; 481 AA.	FT	NON TER 481 481
ANG1	ANG1 BOVIN STANDARD; PRT; 481 AA.	SQ	SEQUENCE 481 AA; 55557 MW; 8EEC9ED84FC2BB50 CRC64;
ANG1	ANG1 BOVIN STANDARD; PRT; 481 AA.	-----	Query Match 80.7%; Score 85.5%; DB 1; Length 481;
ANG1	ANG1 BOVIN STANDARD; PRT; 481 AA.	-----	Best Local Similarity 90.0%; Prod. No. 0.00024;
ANG1	ANG1 BOVIN STANDARD; PRT; 481 AA.	-----	Matches 18; Conservative 1; Mismatches 0; Indels 1; Gaps 18;

Db	264	LCTKE-VLLKGKRGKREBKKPF	282	
<b>RESULT 13</b>				
Q6GNY4	XENLA	XENLA PRELIMINARY;	PRT;	504 AA.
ID				
AC				
DT	05-JUL-2004	(TREMBUREl. 27, Created)		
DT	05-JUL-2004	(TREMBUREl. 27, Last sequence update)		
DT	05-JUL-2004	(TREMBUREl. 27, Last annotation update)		
DE	MGC80788	Protein.		
OS	Xenopus laevis	(African clawed frog).		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Xenopus;			
OC	Xenopodinae; Xenopus; Xenopus.			
OX	NCBI_TaxID:8355;			
RN				
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Spleen;			
RX	MEDLINE=2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,			
RA	Klaussner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.R.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marsusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Blakesley R.W., Tsoi N.T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Pters G.J., Abramson R.D., Mullaney S.J.,			
RA	Bosak S.A., McEwan P.J., McCorman K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muñoz D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman J., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bonifard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalls D.E.,			
RA	Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.,			
RA	"Generation and initial analysis of more than 15,000 full-length human			
RA	and mouse cDNA sequences.";			
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
[2]				
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Spleen;			
RX	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;			
RA	Klein S.L., Straubberg R.L., Wagner L., Pontius J., Clifton S.W.,			
RA	Richardson P.,			
RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus			
RT	initiative."			
RL	Dev. Dyn. 225:384-391 (2002).			
RP				
RC	NUCLEOTIDE SEQUENCE.			
RX	Q6GNY4-XENLA	XENLA PRELIMINARY;	PRT;	504 AA.
RA	Klein S., Gerhard D.S., Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: B0073367; ARH73367.1; -; mRNA.			
DR	GO: GO:0007536; P:Blood coagulation; FEA.			
DR	InterPro: IPR002181; Fibrinogen_C.			
DR	Pfam: PF00147; Fibrinogen_C_1.			
DR	SMART: SM00186; FFG_1.			
DR	PROSITE: PS00514; FIBRIN AG C DOMAIN; 1.			
SQ	SEQUENCE 504 AA, 57797 MW, FA4F7D4174AD390 CRC64;			
Query Match	71.7%	Score 76 DB 2; Length 504;		
Best Local Similarity	70.0%	Pred. No. 0.007; Indels 0; Gaps 0;		
Matches	14; Conservative	Mismatches 3;		
Qy	1 LCTKE-VLLKGKRGKREBKKPF	289		
Db	270 LCSSEGTVKVKKEEEKF	289		

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multiplex capillary sequencer." Genome Res. 10:1757-1771 (2000). [6]

RA NUCLEOTIDE SEQUENCE.  
 RA STRAIN=C57BL/6J; TISSUE=Testis;  
 RA DRINTERPRO; IPR015010; CAG09974.1; -; Genomic\_DNA.  
 RA DRINTERPRO; IPR01827; TF bzZIP.  
 RA DRPFAM; PF07216; bZIP\_2; I.  
 RA DRPROSITE; PS00217; BZIP\_1.  
 RA DRPROSITE; PS00036; BZIP\_BASIC; 1.  
 RA DRDNA-BINDING; Nuclear\_protein.  
 RA DRSEQUENCE 178 AA; 832C61408C134DCP\_CRC64;  
 RA DRSEQUENCE 51.9%; Score 55; DB 2; Length 178;  
 RA DRBEST\_LOCAL\_SIMILARITY 55.6%; Pred. No. 4.1;  
 RA DRMATCHES 10; CONSERVATIVE 3; MISMATCHES 5; INDELS 0; GAPS 0;  
 RA DRQY 2 CTKGVLKGGKRBEBK 19  
 RA DRDB 4 CCEBGVLTAGDKTEKP 21

RA DRSEARCH\_COMPLETED: May 11, 2006, 11:37:15  
 RA DRJOB\_TIME : 237 secs

RA DRSUBMITTED (JUL-2000) to the EMBL/GenBank/DDBJ databases.  
 RA DR ENSEMBL; ENSEMBL0000024280; Mus musculus.  
 RA DR MGI; MGI:1922184; Armc4.  
 RA DRHYPOTHETICAL PROTEIN.  
 RA DRNON\_TER 383 AA; 43608 MN; AA688BA4AACB01D\_CRC64;  
 RA DRSEQUENCE 383 AA; 43608 MN; AA688BA4AACB01D\_CRC64;

RA DRQY 2 CTKGVLKGGKRBEBK 17  
 RA DRDB 262 CSTEGVFLNGKTEEE 277

RA DRQY 2 CTKGVLKGGKRBEBK 17  
 RA DRDB 262 CSTEGVFLNGKTEEE 277

RESULT 15  
 Q4RNQ8\_TETNG  
 ID Q4RNQ8\_TETNG PRELIMINARY;  
 AC Q4RNQ8;  
 DT 13-SEP-2005 (TREMBLrel. 31, Created)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
 DE Chromosome 2 SCAF15010, whole genome shotgun sequence.  
 GN ORFNames=GSTNAME00031451001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontoidae; Tetraodontidae; Tetraodon.  
 OC NCBI\_TaxID=99883;  
 [1]  
 RN NUCLEOTIDE SEQUENCE.  
 RA Jaijlon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N., Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Ricaud S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Baudet N., Castellano S., Anthouard V., Jubin C., Castegnoli V., Katinka M., Vacherie B., Belmont C., Skalli Z., Cattolico L., Poulain J., De Bernardini V., Ra Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J., Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S., Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Laudet V., Schachter V., Queierie F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H., RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype." Nature 431:946-957 (2004). [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RG Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.  
 CC "CARMON. The sequence shown here is derived from an

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: May 11, 2006, 11:37:32 ; Search time 46 Seconds  
(without alignments)

35.946 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKEGVLLKGGKREBKKPF 20

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\*

Maximum Match 100\*

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### ALIGNMENTS

RESULT 1  
US-08-740-223A-7  
; Sequence 7, Application US/08740223A  
; Patent No. 6265564

#### GENERAL INFORMATION:

APPLICANT: Davis, et al.  
TITLE OF INVENTION: Expressed Ligand - Vascular  
TITLE OF INVENTION: Intercellular Signalling Molecule  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
STREET: 777 Old Saw Mill Road  
CITY: Tarrytown  
STATE: NY  
COUNTRY: USA  
ZIP: 10591

#### COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 2.0  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/740,223A  
FILING DATE: 25-OCT-1996  
CLASSIFICATION: 536  
PRIORITY APPLICATION NUMBER: US/02/999  
APPLICATION NUMBER: US/00/22/999  
FILING DATE: 02-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Cobert, Robert J.  
REGISTRATION NUMBER: 36,108  
REFERENCE/DOCKET NUMBER: REG 333  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 914-345-7400  
TELEFAX: 914-345-7721  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 478 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: Mature TLL protein  
LOCATION: 1..478  
OTHER INFORMATION:

US-08-740-223A-7

Query Match Score 106; DB 2; Pred. No. 3..2e-09; Length 478;

Best Local Similarity 100.0%; Score 106; DB 2; Pred. No. 3..2e-09;

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	478	2 US-08-740-223A-7	Sequence 7, Appli
2	106	100.0	478	2 US-09-709-188-7	Sequence 7, Appli
3	106	100.0	478	2 US-10-225-060-7	Sequence 7, Appli
4	106	100.0	495	2 US-08-740-223A-26	Sequence 26, Appli
5	106	100.0	495	2 US-09-709-188-26	Sequence 26, Appli
6	106	100.0	495	2 US-10-225-060-26	Sequence 26, Appli
7	106	100.0	497	2 US-08-740-223A-14	Sequence 14, Appli
8	106	100.0	497	2 US-09-709-188-14	Sequence 14, Appli
9	106	100.0	497	2 US-10-225-060-14	Sequence 14, Appli
10	106	100.0	498	1 US-08-373-579-2	Sequence 2, Appli
11	106	100.0	498	1 US-08-418-595-2	Sequence 2, Appli
12	106	100.0	498	1 US-08-655-926-2	Sequence 2, Appli
13	106	100.0	498	1 US-08-348-492-2	Sequence 2, Appli
14	106	100.0	498	2 US-09-162-437-2	Sequence 2, Appli
15	106	100.0	498	2 US-08-740-223A-2	Sequence 2, Appli
16	106	100.0	498	2 US-08-350-457-20	Sequence 20, Appli
17	106	100.0	498	2 US-09-351-457-2	Sequence 2, Appli
18	106	100.0	498	2 US-09-561-500-2	Sequence 2, Appli
19	106	100.0	498	2 US-09-561-108-2	Sequence 2, Appli
20	106	100.0	498	2 US-09-351-543-2	Sequence 2, Appli
21	106	100.0	498	2 US-09-561-526-2	Sequence 5, Appli
22	106	100.0	498	2 US-09-202-491-5	Sequence 6, Appli
23	106	100.0	498	2 US-09-202-491-6	Sequence 2, Appli
24	106	100.0	498	2 US-08-817-318-2	Sequence 2, Appli
25	106	100.0	498	2 US-09-709-188-2	Sequence 2, Appli
26	106	100.0	498	2 US-09-709-188-20	Sequence 2, Appli
27	106	100.0	498	2 US-09-561-499-2	Sequence 2, Appli

RESULT 2

Query 1 LCTKEGVLLKGGRKEEKPF 20  
Database 244 LCTKEGVLLKGGRKEEKPF 263

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; SEQ ID NO 7

Sequence 7, Application US/09/709/188

Patent No. 6441137

GENERAL INFORMATION

APPLICANT: Davis et al.

TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule

CURRENT APPLICATION NUMBER: US/09/709,188

CURRENT FILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: 08/740,223

PRIOR FILING DATE: 1996-10-25

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7

LENGTH: 478

TYPE: PRT

ORGANISM: Homo sapiens

US-10-789-188-7

Query Match 100.0%; Score 106; DB 2; Length 478;  
Best Local Similarity 100.0%; Pred. No. 3.2e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 LCTKEGVLLKGGRKEEKPF 20  
Database 244 LCTKEGVLLKGGRKEEKPF 263

RESULT 3

Query Match 100.0%; Score 106; DB 2; Length 495;  
Best Local Similarity 100.0%; Pred. No. 3.3e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Patent No. 625008

GENERAL INFORMATION

APPLICANT: Davis et al.

TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule

FILE REFERENCE: REG 333-Z

CURRENT APPLICATION NUMBER: US/10/225,060

CURRENT FILING DATE: 2002-08-21

PRIOR APPLICATION NUMBER: US/09/709,188

PRIOR FILING DATE: 2000-11-09

PRIOR FILING DATE: 1996-10-25

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7

LENGTH: 478

TYPE: PRT

ORGANISM: Homo sapiens

US-10-225-060-7

Query Match 100.0%; Score 106; DB 2; Length 478;  
Best Local Similarity 100.0%; Pred. No. 3.2e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 LCTKEGVLLKGGRKEEKPF 20  
Database 244 LCTKEGVLLKGGRKEEKPF 263

RESULT 4

Query Match 100.0%; Score 106; DB 2; Length 495;  
Best Local Similarity 100.0%; Pred. No. 3.3e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Patent No. 6265564

GENERAL INFORMATION

OTHER INFORMATION: 2N1C1F (chimera 4)  
 US-09-709-188-26  
 Query Match 100.0%: Score 106; DB 2; Length 495;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NO: 261 LCTKEGVLLKGKREEEKPF 280

RESULT 6  
 US-10-225-060-26  
 ; Sequence 26, Application US/10225060  
 ; PATENT NO. 6825008  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Davis et al.  
 ; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling  
 ; FILE REFERENCE: REG 333-Z  
 ; CURRENT FILING DATE: 2002-08-21  
 ; PRIOR APPLICATION NUMBER: US/10/225,060  
 ; PRIOR FILING DATE: 2000-11-09  
 ; PRIOR APPLICATION NUMBER: 08/740,223  
 ; PRIOR FILING DATE: 1996-10-25  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 26  
 ; LENGTH: 495  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Chimeric  
 ; FEATURE:  
 ; OTHER INFORMATION: 2N1C1F (chimera 4)  
 US-10-225-060-26  
 Query Match 100.0%: Score 106; DB 2; Length 495;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 SEQ ID NO: 261 LCTKEGVLLKGKREEEKPF 280

RESULT 7  
 US-08-740-223A-14  
 ; Sequence 14, Application US/08740223A  
 ; PATENT NO. 6265564  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Davis et al.  
 ; TITLE OF INVENTION: Expressed Ligand - Vascular  
 ; NUMBER OF SEQUENCES: 28  
 ; ADDRESSSEE: Regeneron Pharmaceuticals, Inc.  
 ; STREET: 777 Old Saw Mill Road  
 ; CITY: Tarrytown  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10591  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: PasteSEQ Version 2.0  
 ; CURRENT APPLICATION NUMBER:  
 ; FILING DATE: 25-OCT-1996  
 ; CLASSIFICATION:

PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: USSN 60/022/999  
 ; FILING DATE: 02-AUG-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Cobert, Robert J  
 ; REGISTRATION NUMBER: 36,108  
 ; REFERENCE/DOCKET NUMBER: REG 333  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 914-345-7400  
 ; TELEFAX: 914-345-7721  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 497 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FEATURE:  
 ; NAME/KEY: mtl1  
 ; LOCATION: 1..497  
 ; OTHER INFORMATION: mouse TIE-2 ligand 1  
 US-08-740-223A-14  
 Query Match 100.0%: Score 106; DB 2; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LCTKEGVLLKGKREEEKPF 20  
 Db 263 LCTKEGVLLKGKREEEKPF 282

RESULT 8  
 US-09-709-188-14  
 ; Sequence 14, Application US/09709188  
 ; PATENT NO. 644117  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Davis et al.  
 ; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling Molecule  
 ; FILE REFERENCE: REG 333-Z  
 ; CURRENT APPLICATION NUMBER: US/09/709,188  
 ; CURRENT FILING DATE: 2000-11-09  
 ; PRIOR APPLICATION NUMBER: 08/740,223  
 ; PRIOR FILING DATE: 1996-10-25  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SEQ ID NO: 14  
 ; SOFTWARE: PatentIn version 3.1  
 ; LENGTH: 497  
 ; TYPE: PRT  
 ; ORGANISM: Mus sp.  
 US-09-709-188-14  
 Query Match 100.0%: Score 106; DB 2; Length 497;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LCTKEGVLLKGKREEEKPF 20  
 Db 263 LCTKEGVLLKGKREEEKPF 282

RESULT 9  
 US-10-225-060-14  
 ; Sequence 14, Application US/10225060  
 ; PATENT NO. 6825008  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Davis et al.  
 ; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling  
 ; NUMBER OF SEQUENCES: 28  
 ; ADDRESSSEE: Regeneron Pharmaceuticals, Inc.  
 ; STREET: 777 Old Saw Mill Road  
 ; CITY: Tarrytown  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 10591  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: PasteSEQ Version 2.0  
 ; CURRENT APPLICATION NUMBER: US/10/225,060  
 ; CURRENT FILING DATE: 2002-08-21  
 ; PRIOR APPLICATION NUMBER: US/09/709,188

```

; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOs: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 14
; LENGTH: 497
; TYPE: PCT
; ORGANISM: Mus sp.
US-10-225-050-14

Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 LCTKGVLLKGGRREEKPF 20
Db 264 LCTKGVLLKGGRREEKPF 283

RESULT 11
US-08-418-595-2
; Sequence 2, Application US/08418595
; Patent No. 5814464
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,595
; FILING DATE: 06-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,579
; FILING DATE: 17-JAN-1995
; APPLICATION NUMBER: US 08/353,503
; FILING DATE: 09-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,579
; FILING DATE: 17-JAN-1995
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,579
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/353,503
; FILING DATE: 09-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,492
; FILING DATE: 02-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,261
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Cobert, Robert J.
; REGISTRATION NUMBER: 36,108
; REFERENCE/DOCUMENT NUMBER: REG 330-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 345-7400
; FAX: (914) 345-7721
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-418-595-2

Query Match 100.0%; Score 106; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 LCTKGVLLKGGRREEKPF 20
Db 264 LCTKGVLLKGGRREEKPF 283

RESULT 12
US-08-665-926-2
; Query Match 100.0%; Score 106; DB 1; Length 498;

```

Sequence 2, Application US/08665926  
 Patent No. 5851797  
 GENERAL INFORMATION:  
 APPLICANT: Valenzuela et al.  
 TITLE OF INVENTION: TIE LIGAND-3, METHODS OF MAKING AND USES  
 TITLE OF INVENTION: THEREOF  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
 STREET: 777 Old Saw Mill River Road  
 CITY: Tarrytown  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10591-6707  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/665, 926  
 FILING DATE: 19-JUN-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Robert J. Cobert  
 REGISTRATION NUMBER: 36,108  
 REFERENCE/DOCKET NUMBER: REG 330-H  
 TELEPHONE: (914) 345-7400  
 TELEFAX: (914) 345-2113  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 498 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-665-926-2

Query Match 100.0%; Score 106; DB 1; Length 498;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTREGVLKKGKREBEEKPF 20  
 Db 264 LCTREGVLKKGKREBEEKPF 283

RESULT 13  
 US-08-348-492-2  
 Sequence 2, Application US/08348492  
 Patent No. 5879672  
 GENERAL INFORMATION:  
 APPLICANT: Davis, et al.  
 TITLE OF INVENTION: TIE-2 LIGAND, METHOD OF MAKING AND USES  
 TITLE OF INVENTION: THEREOF  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
 STREET: 777 Old Saw Mill River Road  
 CITY: Tarrytown  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10591  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/348, 492  
 FILING DATE: 02-DEC-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/373, 579  
 FILING DATE: 17-JAN-1995  
 APPLICATION NUMBER: US 08/353, 503  
 FILING DATE: 09-DEC-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/348, 492  
 FILING DATE: 02-DEC-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/330, 261  
 FILING DATE: 27-OCT-1994  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/319, 932  
 FILING DATE: 07-OCT-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cobert, Robert J.

REGISTRATION NUMBER: 36,108  
 REFERENCE/DOCKET NUMBER: REG 330-D  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (914) 345-7400  
 TELEFAX: (914) 345-7721  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 498 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-162-437-2

Query Match 100.0%; Score 106; DB 2; Length 498;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-09;  
 Matches 20; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREBKKPF 20  
 Db 264 LCTKEGVLLKGGRREBKKPF 283

Search completed: May 11, 2006, 11:38:49  
 Job time : 46 SECs

---

RESULT 15  
 US-08-740-223A-2  
 Sequence 2, Application US/08740223A  
 Patent No. 6265564

GENERAL INFORMATION:  
 APPLICANT: DAVIS, et al.  
 TITLE OF INVENTION: Expressed Ligand - Vascular  
 Intercellular Signalling Molecule  
 NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Regeneron Pharmaceuticals, Inc.  
 STREET: 777 Old Saw Mill Road  
 CITY: Tarrytown  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10591

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/740-223A  
 FILING DATE: 25-OCT-1996  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 60/022/999  
 FILING DATE: 02-AUG-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Cobert, Robert J  
 REGISTRATION NUMBER: 36,108  
 REFERENCE/DOCKET NUMBER: REG 333

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 914-345-7400  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 498 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 FEATURE:  
 NAME/KEY: Human TIE-2 ligand 1  
 LOCATION: 1..198  
 OTHER INFORMATION: from clone gtl00 encoding htie-2  
 OTHER INFORMATION: ligand 1

US-08-740-223A-2

Query Match 100.0%; Score 106; DB 2; Length 498;

Result No.	Score	Query Match	Length	DB	ID	Description
1	106	100.0	20	4	US-10-789-222-1	Sequence 1, Appli
2	106	100.0	20	4	US-10-789-222-2	Sequence 2, Appli
3	106	100.0	235	3	US-09-832-355A-18	Sequence 18, Appli
4	106	100.0	260	4	US-10-273-180-2	Sequence 2, Appli
5	106	100.0	298	4	US-10-273-180-4	Sequence 4, Appli
6	106	100.0	309	4	US-10-273-180-6	Sequence 6, Appli
7	106	100.0	312	4	US-10-273-180-8	Sequence 8, Appli
8	106	100.0	402	4	US-10-367-259A-36	Sequence 36, Appli
9	106	100.0	402	4	US-10-829-829-115	Sequence 15, Appli
10	106	100.0	456	4	US-10-789-222-7	Sequence 7, Appli
11	106	100.0	456	4	US-10-789-222-8	Sequence 8, Appli
12.	106	100.0	478	4	US-10-225-060-7	Sequence 14, Appli
13.	106	100.0	478	5	US-10-928-911-14	Sequence 14, Appli
14.	106	100.0	478	6	US-11-073-120-7	Sequence 14, Appli
15	106	100.0	495	4	US-10-225-060-16	Sequence 26, Appli
16	106	100.0	495	5	US-10-928-911-26	Sequence 26, Appli
17	106	100.0	495	6	US-11-073-120-26	Sequence 26, Appli
18	106	100.0	497	4	US-10-225-060-14	Sequence 14, Appli
19	106	100.0	497	5	US-10-928-911-14	Sequence 14, Appli
20	106	100.0	497	6	US-11-073-120-14	Sequence 14, Appli
21	106	100.0	498	3	US-09-998-831-2	Sequence 2, Appli
22	106	100.0	498	3	US-09-897-306-13	Sequence 13, Appli
23	106	100.0	498	3	US-09-832-355A-15	Sequence 15, Appli
24	106	100.0	498	3	US-09-998-833-2	Sequence 2, Appli
25	106	100.0	498	4	US-10-179-744-2	Sequence 2, Appli
26	106	100.0	498	4	US-10-186-817-2	Sequence 2, Appli
27	106	100.0	498	4	US-10-215-224-5	Sequence 5, Appli

```

Query Match, Similarity 100.0%; Score 106; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e-01; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NOS: 30
GENERAL INFORMATION:
  APPLICANT: Kovacs, Imre
  ATTORNEY: Kessler, Paul
  TITLE OF INVENTION: VEGF FUSION PROTEINS
  FILE REFERENCE: 205654
  CURRENT APPLICATION NUMBER: US/09/832,355A
  CURRENT FILING DATE: 2001-04-10
  NUMBER OF SEQ ID NOS: 126
  SOFTWARE: PatentIn version 3.0
  SEQ ID NO: 18
  LENGTH: 235
  TYPE: PRT
  ORGANISM: Homo sapiens
US-09-832-355A-18

Query Match, Similarity 100.0%; Score 106; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.2e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NOS: 30
GENERAL INFORMATION:
  APPLICANT: KOH, Gou Young
  TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
  FILE REFERENCE: 10010-00001
  CURRENT APPLICATION NUMBER: US/10/273,180
  CURRENT FILING DATE: 2002-10-18
  NUMBER OF SEQ ID NOS: 30
  SOFTWARE: PatentIn version 3.1
  SEQ ID NO: 6
  LENGTH: 309
  TYPE: PRT
  ORGANISM: Homo sapiens
US-10-273-180-6

Query Match, Similarity 100.0%; Score 106; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NOS: 30
GENERAL INFORMATION:
  APPLICANT: KOH, Gou Young
  TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
  FILE REFERENCE: 10010-00001
  CURRENT APPLICATION NUMBER: US/10/273,180
  CURRENT FILING DATE: 2002-10-18
  NUMBER OF SEQ ID NOS: 30
  SOFTWARE: PatentIn version 3.1
  SEQ ID NO: 4
  LENGTH: 298
  TYPE: PRT
  ORGANISM: Homo sapiens
US-10-273-180-4

Query Match, Similarity 100.0%; Score 106; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.9e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NOS: 30
GENERAL INFORMATION:
  APPLICANT: KOH, Gou Young
  TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
  FILE REFERENCE: 10010-00001
  CURRENT APPLICATION NUMBER: US/10/273,180
  CURRENT FILING DATE: 2002-10-18
  NUMBER OF SEQ ID NOS: 30
  SOFTWARE: PatentIn version 3.1
  SEQ ID NO: 20
  LENGTH: 298
  TYPE: PRT
  ORGANISM: Homo sapiens
US-10-273-180-2

Query Match, Similarity 100.0%; Score 106; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 2.5e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NOS: 30
GENERAL INFORMATION:
  APPLICANT: KOH, Gou Young
  TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
  FILE REFERENCE: 10010-00001
  CURRENT APPLICATION NUMBER: US/10/273,180
  CURRENT FILING DATE: 2002-10-18
  NUMBER OF SEQ ID NOS: 30
  SOFTWARE: PatentIn version 3.1
  SEQ ID NO: 2
  LENGTH: 260
  TYPE: PRT
  ORGANISM: Homo sapiens
US-10-273-180-2

Query Match, Similarity 100.0%; Score 106; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 3e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NOS: 30
GENERAL INFORMATION:
  APPLICANT: KOH, Gou Young
  TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
  FILE REFERENCE: 10010-00001
  CURRENT APPLICATION NUMBER: US/10/273,180
  CURRENT FILING DATE: 2002-10-18
  NUMBER OF SEQ ID NOS: 30
  SOFTWARE: PatentIn version 3.1
  SEQ ID NO: 8
  LENGTH: 312
  TYPE: PRT
  ORGANISM: Homo sapiens
US-10-273-180-8

Query Match, Similarity 100.0%; Score 106; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 3e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NOS: 30
GENERAL INFORMATION:
  APPLICANT: KOH, Gou Young
  TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
  FILE REFERENCE: 10010-00001
  CURRENT APPLICATION NUMBER: US/10/273,180
  CURRENT FILING DATE: 2002-10-18
  NUMBER OF SEQ ID NOS: 30
  SOFTWARE: PatentIn version 3.1
  SEQ ID NO: 20
  LENGTH: 312
  TYPE: PRT
  ORGANISM: Homo sapiens
US-10-273-180-4

Query Match, Similarity 100.0%; Score 106; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 3e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; SEQ ID NOS: 30
GENERAL INFORMATION:
  APPLICANT: KOH, Gou Young
  TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES
  FILE REFERENCE: 10010-00001
  CURRENT APPLICATION NUMBER: US/10/273,180
  CURRENT FILING DATE: 2002-10-18
  NUMBER OF SEQ ID NOS: 30
  SOFTWARE: PatentIn version 3.1
  SEQ ID NO: 78
  LENGTH: 312
  TYPE: PRT
  ORGANISM: Homo sapiens
US-10-273-180-78

```

RESULT 8  
 US-10-367-259A-36  
 ; Sequence 36, Application US/10367259A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ELLIS, LEE M.  
 ; FILE REFERENCE: UTSC:69805  
 ; CURRENT APPLICATION NUMBER: US/10/367,259A  
 ; CURRENT FILING DATE: 2003-02-14  
 ; PRIOR APPLICATION NUMBER: 60/356,809  
 ; PRIOR FILING DATE: 2002-02-14  
 ; NUMBER OF SEQ ID NOS: 56  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 36  
 ; LENGTH: 402  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-367-259A-36

Query Match 100.0%; Score 106; DB 4; Length 402;  
 Best Local Similarity 100.0%; Pred. No. 4e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEKPF 20  
 Db 264 LCTKEGVLLKGGRREEKPF 283

RESULT 9  
 US-11-019-829-115  
 ; Sequence 115, Application US/11019829  
 ; Publication No. US20050134465AA1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hoffmann-La Roche Inc.  
 ; TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat  
 ; FILE REFERENCE: 22304  
 ; CURRENT APPLICATION NUMBER: US/11/019,829  
 ; CURRENT FILING DATE: 2004-12-22  
 ; NUMBER OF SEQ ID NOS: 146  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 115  
 ; LENGTH: 402  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-019-829-115

NAME/KEY: angiopoietin 1 variant 2  
 LOCATION: (1)-(40)  
 OTHER INFORMATION: LocusID: 284; NM\_139290

Query Match 100.0%; Score 106; DB 6; Length 402;  
 Best Local Similarity 100.0%; Pred. No. 4e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEKPF 20  
 Db 264 LCTKEGVLLKGGRREEKPF 283

RESULT 10  
 US-10-789-222-7  
 ; Sequence 7, Application US/10789222  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yu, Qin  
 ; TITLE OF INVENTION: of the same  
 ; FILE REFERENCE: UPN003-10 (P3115)  
 ; CURRENT FILING DATE: 2004-02-27  
 ; PRIOR APPLICATION NUMBER: US/10/789,222  
 ; PRIOR FILING DATE: 2003-02-27

Query Match 100.0%; Score 106; DB 4; Length 456;  
 Best Local Similarity 100.0%; Pred. No. 4e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEKPF 20  
 Db 222 LCTKEGVLLKGGRREEKPF 241

RESULT 11  
 US-10-789-222-8  
 ; Sequence 8, Application US/10789222  
 ; Publication No. US20040186054AA1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yu, Qin  
 ; TITLE OF INVENTION: Angiopoietin and Fragments, Mutants, and Analogs Thereof and Uses  
 ; TITLE OF INVENTION: of the same  
 ; FILE REFERENCE: UPN003-10 (P3115)  
 ; CURRENT APPLICATION NUMBER: US/10/789,222  
 ; CURRENT FILING DATE: 2004-02-27  
 ; PRIOR APPLICATION NUMBER: US 60/450,582  
 ; PRIOR FILING DATE: 2003-02-27  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 8  
 ; LENGTH: 456  
 ; TYPE: PRT  
 ; ORGANISM: mouse  
 US-10-789-222-8

Query Match 100.0%; Score 106; DB 4; Length 456;  
 Best Local Similarity 100.0%; Pred. No. 4e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEKPF 20  
 Db 222 LCTKEGVLLKGGRREEKPF 241

RESULT 12  
 US-10-225-060-7  
 ; Sequence 7, Application US/10225060  
 ; Publication No. US2003002891AA1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Davis et al.  
 ; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling  
 ; TITLE OF INVENTION: Molecule  
 ; FILE REFERENCE: REG 333-Z  
 ; CURRENT APPLICATION NUMBER: US/10/225,060  
 ; CURRENT FILING DATE: 2002-08-21  
 ; PRIOR APPLICATION NUMBER: US/09/709,188  
 ; PRIOR FILING DATE: 2000-11-09  
 ; PRIOR APPLICATION NUMBER: 08/740,223  
 ; PRIOR FILING DATE: 1996-10-25  
 ; NUMBER OF SEQ ID NOS: 30  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 7  
 ; LENGTH: 478  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-225-060-7

Query Match 100.0%; Score 106; DB 4; Length 478;  
 Best Local Similarity 100.0%; Pred. No. 4e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEKEPF 20  
 Db 244 LCTKEGVLLKGGRREEKEPF 263

RESULT 13  
 US-10-928-911-7  
 Sequence 7, Application US/10928911  
 Publication No. US2005010609AA1  
 GENERAL INFORMATION:  
 APPLICANT: Davis, Samuel  
 Yancopoulos, George D.  
 TITLE OF INVENTION: Expressed Ligand - Vascular  
 Intercellular Signaling Molecule  
 FILE REFERENCE: REG 333X  
 CURRENT APPLICATION NUMBER: US/10/928,911  
 CURRENT FILING DATE: 2004-08-27  
 PRIOR APPLICATION NUMBER: 10/1225,060  
 PRIOR FILING DATE: 2002-08-21  
 PRIOR APPLICATION NUMBER: 09/709,188  
 PRIOR FILING DATE: 2000-11-09  
 PRIOR APPLICATION NUMBER: 08/740,223  
 NUMBER OF SEQ ID NOS: 30  
 SOFTWARE: FastaSEQ for Windows Version 4.0  
 SEQ ID NO: 7  
 LENGTH: 478  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-10-928-911-7

Query Match 100.0%; Score 106; DB 5; Length 478;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEKEPF 20  
 Db 244 LCTKEGVLLKGGRREEKEPF 263

Search completed: May 11, 2006, 11:41:41  
 Job time : 167 secs

RESULT 14  
 US-11-073-120-7  
 Sequence 7, Application US/11073120  
 Publication No. US20050186665A1  
 GENERAL INFORMATION:  
 APPLICANT: Davis, Samuel  
 Yancopoulos, George D.  
 TITLE OF INVENTION: Expressed Ligand - Vascular  
 Intercellular Signaling Molecule  
 FILE REFERENCE: REG 333X  
 CURRENT APPLICATION NUMBER: US/11/073,120  
 CURRENT FILING DATE: 2005-03-04  
 PRIOR APPLICATION NUMBER: 10/1225,060  
 PRIOR FILING DATE: 2002-08-21  
 PRIOR APPLICATION NUMBER: 09/709,188  
 PRIOR FILING DATE: 2000-11-09  
 NUMBER OF SEQ ID NOS: 30  
 SOFTWARE: FastaSEQ for Windows Version 4.0  
 SEQ ID NO: 7  
 LENGTH: 478  
 TYPE: PRT  
 ORGANISM: Homo sapien  
 US-11-073-120-7

Query Match 100.0%; Score 106; DB 6; Length 478;  
 Best Local Similarity 100.0%; Pred. No. 4.8e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEKEPF 20  
 Db 244 LCTKEGVLLKGGRREEKEPF 263

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model.

Run on: May 11, 2006, 11:39:02 ; Search time 27 Seconds (without alignments)

34.777 Million cell updates/sec

Title: US-10-789-222-1

Perfect score: 106

Sequence: 1 LCTKEGVLLKGKREBEEKPP 20

Scoring table: BL0SUM62

Gapext 0.0 , Gapext 0.5

Searched: 250354 seqs, 46948837 residues

Total number of hits satisfying chosen parameters: 250354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\_New :\*

1: /SIDSS5/podata/1/pubpa/us08\_new\_pub.pep:\*

2: /SIDSS5/podata/1/pubpa/us06\_new\_pub.pep:\*

3: /SIDSS5/podata/1/pubpa/us07\_new\_pub.pep:\*

4: /SIDSS5/podata/1/pubpa/us08\_new\_pub.pep:\*

5: /SIDSS5/podata/1/pubpa/pct\_new\_pub.pep:\*

6: /SIDSS5/podata/1/pubpa/us05\_new\_pub.pep:\*

7: /SIDSS5/podata/1/pubpa/us09\_new\_pub.pep:\*

8: /SIDSS5/podata/1/pubpa/us10\_new\_pub.pep:\*

9: /SIDSS5/podata/1/pubpa/us10\_new\_pub.pep:\*

10: /SIDSS5/podata/1/pubpa/us11\_new\_pub.pep:\*

11: /SIDSS5/podata/1/pubpa/us11\_new\_pub.pep:\*

12: /SIDSS5/podata/1/pubpa/us06\_new\_pub.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Query	Match	Best Local Matches	Similarity	Score	DB 11
%											Pred. No. 2.3e-09 ; Length 260;
1	106	100.0	260	11	US-11-204-465-2	Sequence 2, Appli	1	LCTKEGVLLKGKREBEEKPP	20	100.0%	Score 106;
2	106	100.0	298	11	US-11-284-465-4	Sequence 4, Appli	20			100.0%	Pred. No. 2.3e-09 ;
3	106	100.0	309	11	US-11-284-465-6	Sequence 6, Appli	20			100.0%	Length 260;
4	106	100.0	312	11	US-11-284-465-8	Sequence 8, Appli	20			100.0%	;
5	106	100.0	498	11	US-11-254-137-2	Sequence 2, Appli	20			100.0%	;
6	96	90.6	495	11	US-11-254-137-5	Sequence 5, Appli	20			100.0%	;
7	89.5	84.4	497	11	US-11-149-462-11	Sequence 11, Appli	20			100.0%	;
8	89.5	84.4	497	11	US-11-098-536-163	Sequence 163, Appli	20			100.0%	;
9	89.5	84.4	497	11	US-11-198-739-163	Sequence 163, Appli	20			100.0%	;
10	45	42.5	482	11	US-11-188-298-21319	Sequence 21319, Appli	20			100.0%	;
11	45	42.5	923	11	US-11-075-047A-113	Sequence 113, Appli	20			100.0%	;
12	44.5	42.0	249	11	US-11-098-568A-24481	Sequence 24481, Appli	20			100.0%	;
13	44.5	42.0	260	11	US-11-096-568A-24480	Sequence 24480, Appli	20			100.0%	;
14	44.5	42.0	354	11	US-11-096-568A-24479	Sequence 24479, Appli	20			100.0%	;
15	44	41.5	275	11	US-11-110-977-2	Sequence 2, Appli	20			100.0%	;
16	44	41.5	282	11	US-11-264-096-458	Sequence 458, Appli	20			100.0%	;
17	44	41.5	318	11	US-11-266-096-455	Sequence 455, Appli	20			100.0%	;
18	44	41.5	798	11	US-11-079-463-10034	Sequence 10034, Appli	20			100.0%	;
19	43	40.6	113	8	US-10-370-959-74	Sequence 74, Appli	20			100.0%	;
20	43	40.6	415	11	US-11-188-946-6	Sequence 6, Appli	20			100.0%	;
21	43	40.6	589	9	US-10-467-657-4826	Sequence 4826, Appli	20			100.0%	;

## ALIGNMENTS

RESULT 1

US-11-284-465-2

; Sequence 2, Application US/11284465

; Publication No. US20060074230A1

; GENERAL INFORMATION:

; APPLICANT: KOH, Gou Young

; TITLE/INVENTION: CHIMERIC COILED COIL MOLECULES

; FILE REFERENCE: 10010-00001

; CURRENT APPLICATION NUMBER: US/11/284,465

; CURRENT FILING DATE: 2005-11-21

; PRIOR APPLICATION NUMBER: US/10/273,180

; PRIOR FILING DATE: 2002-10-18

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO: 2

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-284-465-2

RESULT 2

US-11-284-465-4

; Sequence 4, Application US/11284465

; Publication No. US20060074230A1

; GENERAL INFORMATION:

; APPLICANT: KOH, Gou Young

; TITLE/INVENTION: CHIMERIC COILED COIL MOLECULES

; FILE REFERENCE: 10010-00001

; CURRENT APPLICATION NUMBER: US/11/284,465

; CURRENT FILING DATE: 2005-11-21

; PRIOR APPLICATION NUMBER: US/10/273,180

; PRIOR FILING DATE: 2002-10-18

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

4 ; LENGTH: 298  
 4 ; TYPE: PRT  
 4 ; ORGANISM: *Homo sapiens*  
 US-11-284-465-4

Query Match 100.0%; Score 106; DB 11; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEKPF 20  
 Db 64 LCTKEGVLLKGGRREEKPF 83

RESULT 3  
 US-11-284-465-6  
 Sequence 6, Application US/11284465  
 Publication No. US20060074230A1  
 GENERAL INFORMATION:  
 APPLICANT: KOH, Gou Young  
 TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES  
 FILE REFERENCE: 10010-00001  
 CURRENT APPLICATION NUMBER: US/11/284,465  
 CURRENT FILING DATE: 2005-11-21  
 PRIOR APPLICATION NUMBER: US/10/273,180  
 PRIOR FILING DATE: 2002-10-18  
 NUMBER OF SEQ ID NOS: 30  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 6  
 LENGTH: 309  
 TYPE: PRT  
 ORGANISM: *Homo sapiens*

Query Match 100.0%; Score 106; DB 11; Length 309;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEKPF 20  
 Db 75 LCTKEGVLLKGGRREEKPF 94

RESULT 4  
 US-11-284-465-8  
 Sequence 8, Application US/11284465  
 Publication No. US20060074230A1  
 GENERAL INFORMATION:  
 APPLICANT: KOH, Gou Young  
 TITLE OF INVENTION: CHIMERIC COILED COIL MOLECULES  
 FILE REFERENCE: 10010-00001  
 CURRENT APPLICATION NUMBER: US/11/284,465  
 CURRENT FILING DATE: 2005-11-21  
 PRIOR APPLICATION NUMBER: US/10/273,180  
 PRIOR FILING DATE: 2002-10-18  
 NUMBER OF SEQ ID NOS: 30  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 8  
 LENGTH: 312  
 TYPE: PRT  
 ORGANISM: *Homo sapiens*  
 US-11-284-465-8

Query Match 100.0%; Score 106; DB 11; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEKPF 20  
 Db 78 LCTKEGVLLKGGRREEKPF 97

RESULT 5  
 US-11-254-137-2  
 Sequence 2, Application US/11254137  
 Publication No. US20060083745A1  
 GENERAL INFORMATION:  
 APPLICANT: RAN, PHILIP E.  
 TITLE OF INVENTION: CANCER TREATMENT KITS COMPRISING THERAPEUTIC CONJUGATES  
 FILE REFERENCE: 4001.002383  
 CURRENT APPLICATION NUMBER: US/11/254,137  
 CURRENT FILING DATE: 2005-10-19  
 PRIOR APPLICATION NUMBER: US/09/351,149  
 PRIOR FILING DATE: 1999-07-12  
 NUMBER OF SEQ ID NOS: 5  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 2  
 LENGTH: 498  
 TYPE: PRT  
 ORGANISM: *Homo sapiens*  
 US-11-254-137-2

Query Match 100.0%; Score 106; DB 11; Length 498;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEKPF 20  
 Db 264 LCTKEGVLLKGGRREEKPF 283

RESULT 6  
 US-11-254-137-5  
 Sequence 5, Application US/11254137  
 Publication No. US20060083745A1  
 GENERAL INFORMATION:  
 APPLICANT: RAN, PHILIP E.  
 TITLE OF INVENTION: CANCER TREATMENT KITS COMPRISING THERAPEUTIC CONJUGATES  
 FILE REFERENCE: 4001.002383  
 CURRENT APPLICATION NUMBER: US/11/254,137  
 CURRENT FILING DATE: 2005-10-19  
 PRIOR APPLICATION NUMBER: US/09/351,149  
 PRIOR FILING DATE: 1999-07-12  
 NUMBER OF SEQ ID NOS: 5  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 5  
 LENGTH: 495  
 TYPE: PRT  
 ORGANISM: *Homo sapiens*  
 US-11-254-137-5

Query Match 100.0%; Score 106; DB 11; Length 495;  
 Best Local Similarity 95.0%; Pred. No. 1.8e-07;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LCTKEGVLLKGGRREEKPF 20  
 Db 261 LSTKEGVLLKGGRREEKPF 280

RESULT 7  
 US-11-149-462-11  
 Sequence 11, Application US/11149462  
 Publication No. US2006002978A1  
 GENERAL INFORMATION:  
 APPLICANT: Shea, Lonnie D.  
 APPLICANT: Shea, Lonnie L.  
 APPLICANT: Whittlesey, Kevin  
 APPLICANT: Yang, Yang  
 APPLICANT: Rives, Christopher  
 APPLICANT: Rovedo, Mark  
 APPLICANT: Iskandar, Bermans

/\* TITLE OF INVENTION: Biodegradable Scaffolds and Uses Thereof  
 /\* FILE REFERENCE: 1720-1-011N  
 /\* CURRENT APPLICATION NUMBER: US11/149,462  
 /\* PRIORITY FILING DATE: 2005-06-09  
 /\* PRIORITY APPLICATION NUMBER: 60/578,785  
 /\* PRIORITY FILING DATE: 2004-06-10  
 /\* NUMBER OF SEQ ID NOS: 12  
 /\* SOFTWARE: FastSEQ for Windows Version 4.0  
 /\* SEQ ID NO 11  
 /\* LENGTH: 497  
 /\* TYPE: PRT  
 /\* ORGANISM: Homo sapiens  
 US-11-149-462-11

Query Match 84.4%; Score 89.5; DB 11; Length 497;  
 Best Local Similarity 95.0%; Pred. No. 2e-06;  
 Matches 19; Conservative 0; Mismatches 0;  
 Indels 1; Gaps 1;  
 Qy 1 LCTKEGVLLKGGRKEEKPF 20  
 Db 264 LCTKE-VLLKGGRKEEKPF 282

RESULT 8  
 US-11-049-536-163  
 Sequence 163, Application US/11049536  
 Publication No. US20060024297A1  
 GENERAL INFORMATION:  
 APPLICANT: Wood, Clive R.  
 Dransfield, Daniel T.  
 Pieters, Henk  
 HOET, Rene  
 APPLICANT: Hufton, Simon E.  
 FILE REFERENCE: 10280-128001  
 CURRENT APPLICATION NUMBER: US/11/049,536  
 PRIORITY APPLICATION NUMBER: 2004-08-12  
 PRIORITY FILING DATE: 2003-08-12  
 CURRENT FILING DATE: 2005-02-02  
 NUMBER OF SEQ ID NOS: 721  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO 163  
 LENGTH: 497  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-049-536-163

Query Match 84.4%; Score 89.5; DB 11; Length 497;  
 Best Local Similarity 95.0%; Pred. No. 2e-06;  
 Matches 19; Conservative 0; Mismatches 0;  
 Indels 1; Gaps 1;

Qy 1 LCTKEGVLLKGGRKEEKPF 20  
 Db 264 LCTKE-VLLKGGRKEEKPF 282

RESULT 9  
 US-11-199-739-163  
 Sequence 163, Application US/11199739  
 Publication No. US20060037138A1  
 GENERAL INFORMATION:  
 APPLICANT: Wood, Clive R.  
 Dransfield, Daniel T.  
 Pieters, Henk  
 HOET, Rene  
 APPLICANT: Hufton, Simon E.  
 FILE REFERENCE: 10280-135001  
 CURRENT APPLICATION NUMBER: US/11/199,739  
 CURRENT FILING DATE: 2005-08-09  
 PRIORITY APPLICATION NUMBER: US 11/049,536  
 LENGTH: 497  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-075-047A-113

Query Match 84.4%; Score 89.5; DB 11; Length 497;  
 Best Local Similarity 95.0%; Pred. No. 2e-06;  
 Matches 19; Conservative 0; Mismatches 0;  
 Indels 1; Gaps 1;  
 Qy 1 LCTKEGVLLKGGRKEEKPF 20  
 Db 264 LCTKE-VLLKGGRKEEKPF 282

RESULT 10  
 US-11-188-298-21319  
 Sequence 21319, Application US/11188298  
 Publication No. US20060075522A1  
 GENERAL INFORMATION:  
 APPLICANT: Abad, Mark S. et al.  
 FILE REFERENCE: 38-21(5452)B  
 CURRENT APPLICATION NUMBER: US/11/188,298  
 PRIORITY APPLICATION NUMBER: 60/592,978  
 PRIORITY FILING DATE: 2005-07-22  
 NUMBER OF SEQ ID NOS: 22569  
 SEQ ID NO 21319  
 LENGTH: 482  
 TYPE: PRT  
 ORGANISM: Geobacillus stearothermophilus  
 US-11-188-298-21319

Query Match 42.5%; Score 45; DB 11; Length 482;  
 Best Local Similarity 75.0%; Pred. No. 25;  
 Matches 9; Conservative 2; Mismatches 1;  
 Indels 0; Gaps 0;  
 Qy 6 GVLLKGGRKEE 17  
 Db 340 GVLLKGGRMKE 351

RESULT 11  
 US-11-075-047A-113  
 Sequence 113, Application US/11075047A  
 Publication No. US2006030000A1  
 GENERAL INFORMATION:  
 APPLICANT: ALITALO, et al.  
 FILE REFERENCE: 28967/33700A  
 CURRENT APPLICATION NUMBER: US/11/075,047A  
 PRIORITY APPLICATION NUMBER: US 60/550,907  
 NUMBER OF SEQ ID NOS: 128  
 PRIORITY FILING DATE: 2004-03-07  
 NUMBER OF SEQ ID NOS: 128  
 SEQ ID NO 113  
 LENGTH: 923  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-11-075-047A-113

Query Match 42.5%; Score 45; DB 11; Length 923;  
 Best Local Similarity 46.7%; Pred. No. 51;  
 Matches 7; Conservative 4; Mismatches 4;  
 Indels 0; Gaps 0;

Qy 6 GVLKGGKRAEKEKPF 20  
 Db 497 GIIIQGKAKRENKVF 511

RESULT 12  
 US-11-096-568A-24481  
 Sequence 24481, Application US/11096568A  
 Publication No. US20060048240A1  
 GENERAL INFORMATION:  
 APPLICANT: Alexandrov, Nickolai et al.  
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
 FILE REFERENCE: 2750-1592PUS2  
 CURRENT APPLICATION NUMBER: US/11/096,568A  
 CURRENT FILING DATE: 2005-04-01  
 NUMBER OF SEQ ID NOS: 34471  
 SEQ ID NO 24481  
 LENGTH: 249  
 TYPE: PRT  
 ORGANISM: *Zea mays* subsp. *mays*  
 FEATURE: NAME/KEY: misc\_feature  
 LOCATION: (1)..(29)  
 OTHER INFORMATION: Ceres Seq. ID no. 12435351

US-11-096-568A-24481  
 Query Match 42.0%; Score 44.5; DB 11; Length 249;  
 Best Local Similarity 37.5%; Pred. No. 15; Indels 1;  
 Matches 12; Conservative 2; Mismatches 3; Gaps 1;

Qy 3 TKEGVVLIK-----GGKREEEKPF 19  
 Db 44 TKEGVVLIK-----GGKREEEKPF 75

RESULT 13  
 US-11-096-568A-24480  
 Sequence 24480, Application US/11096568A  
 Publication No. US20060048240A1  
 GENERAL INFORMATION:  
 APPLICANT: Alexandrov, Nickolai et al.  
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
 FILE REFERENCE: 2750-1592PUS2  
 CURRENT APPLICATION NUMBER: US/11/096,568A  
 CURRENT FILING DATE: 2005-04-01  
 NUMBER OF SEQ ID NOS: 34471  
 SEQ ID NO 24480  
 LENGTH: 260  
 TYPE: PRT  
 ORGANISM: *Zea mays* subsp. *mays*  
 FEATURE: NAME/KEY: misc\_feature  
 LOCATION: (1)..(26)  
 OTHER INFORMATION: Ceres Seq. ID no. 12435350

US-11-096-568A-24480  
 Query Match 42.0%; Score 44.5; DB 11; Length 260;  
 Best Local Similarity 37.5%; Pred. No. 16; Indels 1;  
 Matches 12; Conservative 2; Mismatches 3; Gaps 1;

Qy 3 TKEGVVLIK-----GGKREEEKPF 19  
 Db 55 TKEGVVLIK-----GGKREEEKPF 86

RESULT 14  
 US-11-096-568A-24479  
 Sequence 24479, Application US/11096568A  
 Publication No. US20060048240A1  
 GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.  
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
 TITLE OF INVENTION: *Zea mays* subsp. *mays*  
 FILE REFERENCE: 2750-1592PUS2  
 CURRENT APPLICATION NUMBER: US/11/096,568A  
 CURRENT FILING DATE: 2005-04-01  
 NUMBER OF SEQ ID NOS: 34471  
 SEQ ID NO 24479  
 LENGTH: 354  
 TYPE: PRT  
 ORGANISM: *Zea mays* subsp. *mays*  
 FEATURE: NAME/KEY: misc\_feature  
 LOCATION: (1)..(354)  
 OTHER INFORMATION: Ceres Seq. ID no. 12435349  
 US-11-096-568A-24479  
 Query Match 42.0%; Score 44.5; DB 11; Length 354;  
 Best Local Similarity 37.5%; Pred. No. 22; Mismatches 3; Indels 15; Gaps 1;  
 Matches 12; Conservative 2; Mismatches 3; Indels 15; Gaps 1;

Qy 3 TKEGVVLIK-----GGKREEEKPF 19  
 Db 149 TKEGVVLIK-----GGKREEEKPF 180

RESULT 15  
 US-11-110-977-2  
 Sequence 2, Application US/11110977  
 Publication No. US20050260682A1  
 GENERAL INFORMATION:  
 APPLICANT: Charmley, Patrick R.  
 APPLICANT: Smith, Ryan C.  
 APPLICANT: Argonza-Barrett, Rhodora H.  
 APPLICANT: Fitzgibbon, Matthew P.  
 APPLICANT: Wang, Kai P.  
 TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Peoriasis  
 FILE REFERENCE: CEC118764  
 CURRENT APPLICATION NUMBER: US/11/110,977  
 CURRENT FILING DATE: 2005-04-19  
 PRIORITY NUMBER: US/10/112,645  
 PRIOR FILING DATE: 2002-03-28  
 PRIORITY NUMBER: US 60/280,514  
 PRIOR FILING DATE: 2001-03-29  
 NUMBER OF SEQ ID NOS: 9  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 2  
 LENGTH: 275  
 TYPE: PRT  
 ORGANISM: *Homo sapiens*  
 US-11-110-977-2  
 Query Match 41.5%; Score 44; DB 11; Length 275;  
 Best Local Similarity 52.9%; Pred. No. 20; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LCTKEGVVLIKGGKREEE 17  
 Db 254 LCSSEVGLKNAEQQ 270

Search completed: May 11, 2006, 11:42:14  
 Job time : 28 secs